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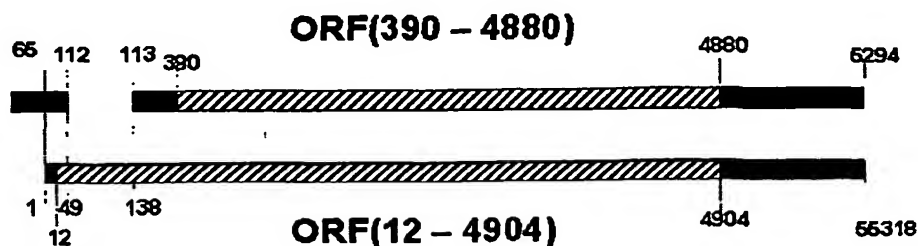
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(54) Title: GENE FAMILIES ASSOCIATED WITH CANCERS



Clone A

Clone B

(57) Abstract: The invention relates generally to the changes in gene expression in human tissues from cancer patients. The invention relates specifically to human gene families which are differentially expressed in cancer tissues of breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach compared to corresponding normal tissues.

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GENE FAMILIES ASSOCIATED WITH CANCERS

FIELD OF THE INVENTION

5 The present invention relates to the changes in gene expression in human tissues from cancer patients. The invention specifically relates to human genes which are differentially expressed in cancer tissues of breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach compared to corresponding normal tissues.

BACKGROUND OF THE INVENTION

10 In the United States, more than one million new cancer cases are diagnosed and about half million people die of cancer. The causes of cancer are many and varied, and include genetic predisposition, environmental influences, infectious agents and ageing. These transform normal cells into cancerous ones by derailing a wide spectrum of regulatory and downstream effector pathways. Several essential alterations in cell
15 physiology collectively dictate malignant growth: self-sufficiency in growth signals, insensitivity to growth-inhibitory signals, evasion of programmed cell death, limitless replicative potential, sustained angiogenesis, and tissue invasion and metastasis (Hanahan and Weinberg (2000), *Cell* 100:57-70).

To date, researchers have been able to identify many genetic alterations believed to
20 underlie tumor development. These genetic alterations include amplification of oncogenes and mutations that result in the loss of tumor suppressor genes. Oncogenes were initially identified as genes carried by viruses that cause transformation of their target cells. A major class of the viral oncogenes have cellular counterparts that are involved in normal cell functions. The cellular genes are called proto-oncogene, and in certain cases their
25 mutation or aberrant in the cell is associated with tumor formation. The generation of a

oncogene represents a gain-of-function in which a cellular proto-oncogene is inappropriately activated. This can involve a mutational change in the protein, or constitutive activation, over-expression, or failure to turn off expression at the appropriate time. About 100 oncogenes have been identified. Examples of oncogenes include, but are not limited to, ras, fos, myc, abl, and myb (Ponder (2001), *Nature* 411:336-341). Tumor suppressor genes, in their wild-type alleles, express proteins that suppress abnormal cellular proliferation. When the gene coding for a tumor suppressor protein is mutated or deleted, the resulting mutant protein or the complete lack of tumor suppressor protein expression may fail to correctly regulate cellular proliferation, and abnormal proliferation may take place, particularly if there is already existing damage to the cellular regulatory mechanism. A number of well-studied human tumors and tumor cell lines have missing or non-functional tumor suppressor genes. Examples of tumor suppressor genes include, but are not limited to, the retinoblastoma susceptibility gene or RB gene, the p53 gene, the deletion in colon carcinoma (DCC) gene and the neurofibromatosis type 1 (NF-1) tumor suppressor gene (Weinberg (1991), *Science* 254:1138-1146). Loss-of-function or inactivation of tumor suppressor genes may play a central role in the initiation and/or progression of a significant number of human cancers.

The utilization of genome-wide expression profiles to classify tumors, to identify drug targets, to identify diagnostic markers and/or to gain further insights into the consequences of chemotherapeutic treatments could facilitate the design of more efficacious stratagems for treating a variety of cancers. Initial studies utilizing gene expression patterns to identify subtypes of cancer produced rather intriguing results (see Perou *et al.* (1999), *Proc Natl Acad Sci U S A* 96:9212-9217; Golub *et al.* (1999), *Science* 286:531-537; Alizadeh *et al.* (2000), *Nature* 403:503-511; Alon *et al.* (1999), *Proc Natl Acad Sci U S A* 96:6745-6750; and Bittner *et al.* (2000), *Nature* 406:536-540; Perou *et al.* (2000), *Nature* 406:747-752). Molecular classification of B-cell lymphoma by gene expression profiling elucidated clinically distinct diffuse large-B-cell lymphoma subgroups (see Alizadeh *et al.*, *supra*). In breast cancer, studies utilizing limited numbers

of genes (8,102 genes) have classified tumors into subtypes based on gene expression profiles, and this study indicated a diversity of molecular phenotypes associated with breast tumors (see Perou *et al.*, supra). In addition, the expression profiling has enabled researchers to map tissue-specific expression levels for thousands of genes (Alon *et al.* 5 (1999), *Proc Natl Acad Sci USA* 96:6745-6750; Iyer *et al.* (1999), *Science* 283:83-87; Khan *et al.* (1998), *Cancer Res* 58:5009-5013; Lee *et al.* (1999), *Science* 285:1390-1393; Wang *et al.* (1999), *Gene* 229:101-108; Whitney *et al.* (1999), *Ann Neurol* 46:425-428). Although these studies have demonstrated that expression profiling may be used to produce improvements in diagnosis of human diseases such as cancer, as well as in the 10 development of improved therapeutic strategies, further studies are needed.

Although cancers are diverse and heterogeneous as they are derived from numerous tissues and multiple etiologic factors, it has been suggested that underlying this variability lies a relatively small number of critical events whose convergence is required for the development of any and all cancers (Evan and Vousden (2001), *Nature* 411:342- 15 348). Accordingly, there exists a need for the comprehensive investigation of the changes in global gene expression levels in many different types of cancers to identify critical molecular markers associated with the development and progression of cancer. There remains a need in the art for materials and methods that permit a more accurate diagnosis of cancer. In addition, there remains a need in the art for methods to treat and methods to 20 identify agents that can effectively treat this disease. The present invention meets these and other needs.

SUMMARY OF THE INVENTION

The present invention is based on new genes that are differentially expressed in cancer tissues compared to normal tissues, hereinafter LFG1, LFG2, LFG3, LFG4, LFG5, 25 LFG6, respectively. The invention includes isolated nucleic acid molecules comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 or the complement thereof.

The present invention further includes the nucleic acid molecules operably linked to one or more expression control elements, including vectors comprising the isolated nucleic acid molecules. The invention further includes host cells transformed to contain the nucleic acid molecules of the invention and methods for producing a protein
5 comprising the step of culturing a host cell transformed with a nucleic acid molecule of the invention under conditions in which the protein is expressed.

The invention further provides an isolated polypeptide selected from the group consisting of an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising a fragment of at least 10
10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and an isolated polypeptide comprising naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Polypeptides of the invention also include polypeptides with an amino acid sequence having at least about 50%, 60%, 70%
15 or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

The present invention further provides methods of identifying other members of
20 the polypeptide family of the invention. Specifically, the nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 can be used as a probe, or to generate PCR primers, in methods to identify nucleic acid molecules that encode other members of the LFG1, LFG2, LFG3, LFG4, LFG5 or LFG6 family of proteins.

The invention further provides an isolated antibody or antigen-binding antibody
25 fragment that specifically binds to a polypeptide of the invention, including monoclonal and polyclonal antibodies.

The invention further provides methods of identifying an agent which modulates the expression of a nucleic acid molecule encoding a protein of the invention, comprising: exposing cells which express the nucleic acid molecule to the agent; and determining whether the agent modulates expression of said nucleic acid molecule, thereby identifying
5 an agent which modulates the expression of a nucleic acid molecule encoding the protein.

The invention further provides methods of identifying an agent which modulates the level of or at least one activity of a protein of the invention, comprising: exposing cells which express the protein to the agent; and determining whether the agent modulates the level of or at least one activity of said protein, thereby identifying an agent which
10 modulates the level of or at least one activity of the protein.

The present invention further provides methods of modulating the expression of a nucleic acid molecule encoding a protein of the invention, comprising the step of administering an effective amount of an agent which modulates the expression of a nucleic acid molecule encoding the protein. The invention also provides methods of modulating
15 at least one activity of a protein of the invention, comprising the step of administering an effective amount of an agent which modulates at least one activity of the protein of the invention.

The invention further provides methods of identifying binding partners for a protein of the invention, comprising the steps of exposing said protein to a potential
20 binding partner; and determining if the potential binding partner binds to said protein, thereby identifying binding partners for the protein.

The present invention further provides methods to identify agents that can block or modulate the association of a protein of the invention with a binding partner. Specifically, an agent can be tested for the ability to block, reduce or otherwise modulate the
25 association of a protein of invention with a binding partner by contacting said protein, or a fragment thereof, and a binding partner with a test agent and determining whether the test agent blocks or reduces the binding of the protein of invention to the binding partner.

The present invention further provides methods for reducing or blocking the association of a protein of invention with one or more of its binding partners, comprising the step of administering an effective amount of an agent which reduces or blocks the binding of said protein to the binding partner. The method can utilize an agent that binds
5 to the protein of invention or to the binding partner.

In accordance with another aspect of the invention, the proteins of the invention can be used as starting points for rational drug design to provide ligands, therapeutic drugs or other types of small chemical molecules. Alternatively, small molecules or other compounds identified by the above-described screening assays may serve as “lead
10 compounds” in rational drug design.

The present invention further relates to a process for treating cancer comprising inserting into a cancerous cell a nucleic acid construct comprising the nucleic acid molecules of the invention operably linked to a promoter or enhancer element such that expression of said nucleic acid molecule causes suppression of said cancer.

15 The present invention further includes non-human transgenic animals modified to contain the nucleic acid molecules of the invention, or non-human transgenic animals modified to contain the mutated nucleic acid molecules such that expression of the encoded polypeptides of the invention is prevented.

The present invention also includes non-human transgenic animals in which all or
20 a portion of a gene comprising all or a portion of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 has been knocked out or deleted from the genome of the animal.

The invention further provides methods of diagnosing cancers, comprising the steps of acquiring a tissue, blood, urine or other sample from a subject and determining the level of expression of a nucleic acid molecule of the invention or polypeptide of the
25 invention.

The invention further includes compositions comprising a diluent and a polypeptide or protein selected from the group consisting of an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising a fragment of at least 10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and an isolated polypeptide with an amino acid sequence having at least about 50%, 60%, 70% or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the relative alignment positions of the two LFG1 clones.

Figure 2 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG1-Clone A (SEQ ID NO: 2). Analysis was performed according to the method of Kyte-Doolittle.

Figure 3 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG1-Clone B (SEQ ID NO: 4). Analysis was performed according to the method of Kyte-Doolittle.

Figure 4 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG2 (SEQ ID NO: 6). Analysis was performed according to the method of Kyte-Doolittle.

Figure 5 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG3 (SEQ ID NO: 8). Analysis was performed according to the method of Kyte-Doolittle.

Figure 6 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG4 (SEQ ID NO: 10). Analysis was performed according to the method of Kyte-Doolittle.

Figure 7 is a hydrophobicity plot of the protein encoded by the open reading frame of ALFG5 (SEQ ID NO: 12). Analysis was performed according to the method of Kyte-Doolittle.

Figure 8 shows the relative alignment positions of the two LFG6 clones.

Figure 9 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG6-#20 (SEQ ID NO: 14). Analysis was performed according to the method of Kyte-Doolittle.

Figure 10 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG6-#46 (SEQ ID NO: 16). Analysis was performed according to the method of Kyte-Doolittle.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

I. General Description

The present invention is based in part on the identification of new gene families that are differentially expressed in cancerous human tissues compared to normal human tissues. These gene families correspond to the human cDNA of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 and 15.

The genes and proteins of the invention may be used as diagnostic agents or markers to detect cancer or to differentiate carcinoma from normal tissue in a sample. They can also serve as a target for agents that modulate gene expression or activity. For example, agents may be identified that modulate biological processes associated with tumor growth, including the hyperplastic process of cancer.

II. Specific Embodiments

A. The Proteins Associated with Cancer

The present invention provides isolated proteins, allelic variants of the proteins, and conservative amino acid substitutions of the proteins. As used herein, the “protein” or “polypeptide” refers, in part, to a protein that has the human amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. The terms also refer to naturally occurring allelic variants and proteins that have a slightly different amino acid sequence than that specifically recited above. Allelic variants, though possessing a slightly different amino acid sequence than those recited above, will still have the same or similar biological functions associated with these proteins.

As used herein, the family of proteins related to the human amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 refers to proteins that have been isolated from organisms in addition to humans. The methods used to identify and isolate other members of the family of proteins related to these proteins are described below.

The proteins of the present invention are preferably in isolated form. As used herein, a protein is said to be isolated when physical, mechanical or chemical methods are employed to remove the protein from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated protein.

The proteins of the present invention further include insertion, deletion or conservative amino acid substitution variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. As used herein, a conservative variant refers to alterations in the amino acid sequence that do not adversely affect the biological functions of the protein. A substitution, insertion or deletion is said to adversely affect the protein when the altered sequence prevents or disrupts a biological function associated with the protein. For example, the overall charge, structure or hydrophobic/hydrophilic properties of the protein, in certain instances, may be altered without adversely affecting a biological activity. Accordingly, the amino acid sequence can be altered, for example to render the peptide more hydrophobic or hydrophilic, without adversely affecting the biological activities of the protein.

Ordinarily, the allelic variants, the conservative substitution variants, and the members of the protein family, will have an amino acid sequence having at least about 50%, 60%, 70% or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, more preferably at least about 80%, even more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity. Identity or homology with respect to such sequences is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity (see section B for the relevant parameters). Fusion proteins, or N-terminal, C-terminal or internal extensions, deletions, or insertions into the peptide sequence shall not be construed as affecting homology.

Thus, the proteins of the present invention include molecules having the amino acid sequence disclosed in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; fragments thereof having a consecutive sequence of at least about 3, 4, 5, 6, 10, 15, 20, 25, 30, 35 or more amino acid residues of these proteins; amino acid sequence variants wherein one or more amino acid residues has been inserted N- or C-terminal to, or within, the disclosed coding sequence; and amino acid sequence variants of the disclosed sequence, or their fragments

as defined above, that have been substituted by at least one residue. Such fragments, also referred to as peptides or polypeptides, may contain antigenic regions, functional regions of the protein identified as regions of the amino acid sequence which correspond to known protein domains, as well as regions of pronounced hydrophilicity. The regions are all easily identifiable by using commonly available protein sequence analysis software such as MacVector (Oxford Molecular).

Contemplated variants further include those containing predetermined mutations by, *e.g.*, homologous recombination, site-directed or PCR mutagenesis, and the corresponding proteins of other animal species, including but not limited to rabbit, mouse, rat, porcine, bovine, ovine, equine and non-human primate species, and the alleles or other naturally occurring variants of the family of proteins; and derivatives wherein the protein has been covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid (for example a detectable moiety such as an enzyme or radioisotope).

The present invention further provides compositions comprising a protein or polypeptide of the invention and a diluent. Suitable diluents can be aqueous or non-aqueous solvents or a combination thereof, and can comprise additional components, for example water-soluble salts or glycerol, that contribute to the stability, solubility, activity, and/or storage of the protein or polypeptide.

As described below, members of the families of proteins can be used: (1) to identify agents which modulate the level of or at least one activity of the protein, (2) to identify binding partners for the protein, (3) as an antigen to raise polyclonal or monoclonal antibodies, (4) as a therapeutic agent or target and (5) as a diagnostic agent or marker of cancer.

B. Nucleic Acid Molecules

The present invention further provides nucleic acid molecules that encode the protein having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and the related proteins herein described, preferably in isolated form. As used herein, "nucleic acid" is defined as RNA or DNA that encodes a protein or peptide as defined above, is complementary to a nucleic acid sequence encoding such peptides, hybridizes to the nucleic acid of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 and remains stably bound to it under appropriate stringency conditions, encodes a polypeptide sharing at least about 50%, 60%, 70% or 75%, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% or more identity with the peptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 or exhibits at least 50%, 60%, 70% or 75%, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% or more nucleotide sequence identity over the open reading frames of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15.

The present invention further includes isolated nucleic acid molecules that specifically hybridize to the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, particularly molecules that specifically hybridize over the open reading frames. Such molecules that specifically hybridize to the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 typically do so under stringent hybridization conditions.

Specifically contemplated are genomic DNA, cDNA, mRNA and antisense molecules, as well as nucleic acids based on alternative backbones or including alternative bases, whether derived from natural sources or synthesized. Such hybridizing or complementary nucleic acids, however, are defined further as being novel and unobvious over any prior art nucleic acid including that which encodes, hybridizes under appropriate stringency conditions, or is complementary to nucleic acid encoding a protein according to the present invention.

Homology or identity at the nucleotide or amino acid sequence level is determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn and tblastx (Altschul *et al.* (1997), *Nucleic*

Acids Res. 25: 3389-3402, and Karlin *et al.* (1990), *Proc. Natl. Acad. Sci. USA* 87: 2264-2268, both fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments, with and without gaps, between a query sequence and a database sequence, then to
5 evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.* (1994), *Nat. Genet.* 6: 119-129 which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (*i.e.*, the statistical significance
10 threshold for reporting matches against database sequences), cutoff, matrix and filter (low complexity) are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff *et al.* (1992), *Proc. Natl. Acad. Sci. USA* 89: 10915-10919, fully incorporated by reference), recommended for query sequences over 85 nucleotides or amino acids in length.

15 For blastn, the scoring matrix is set by the ratios of M (*i.e.*, the reward score for a pair of matching residues) to N (*i.e.*, the penalty score for mismatching residues), wherein the default values for M and N are 5 and -4, respectively. Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the
20 window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

25 "Stringent conditions" are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% SDS at 50°C, or (2) employ during hybridization a denaturing agent such as formamide, for

example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is hybridization in 50% formamide, 5× SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 5 SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2× SSC and 0.1% SDS. A skilled artisan can readily determine and vary the stringency conditions appropriately to obtain a clear and detectable hybridization signal. Preferred molecules are those that hybridize under the above conditions to the complement of SEQ ID NO: 1, 3, 10 5, 7, 9, 11, 13 or 15 and which encode a functional or full-length protein. Even more preferred hybridizing molecules are those that hybridize under the above conditions to the complement strand of the open reading frame of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15.

As used herein, a nucleic acid molecule is said to be "isolated" when the nucleic acid molecule is substantially separated from contaminant nucleic acid molecules encoding other polypeptides. 15

The present invention further provides fragments of the disclosed nucleic acid molecules. As used herein, a fragment of a nucleic acid molecule refers to a small portion of the coding or non-coding sequence. The size of the fragment will be determined by the intended use. For example, if the fragment is chosen so as to encode an active portion of the protein, the fragment will need to be large enough to encode the functional region(s) of the protein. For instance, fragments which encode peptides corresponding to predicted antigenic regions may be prepared. If the fragment is to be used as a nucleic acid probe or PCR primer, then the fragment length is chosen so as to obtain a relatively small number of false positives during probing/priming (see the discussion in Section G). 20

Fragments of the nucleic acid molecules of the present invention (*i.e.*, synthetic oligonucleotides) that are used as probes or specific primers for the polymerase chain reaction (PCR), or to synthesize gene sequences encoding proteins of the invention, can 25

easily be synthesized by chemical techniques, for example, the phosphoramidite method of Matteucci *et al.*, ((1981) *J. Am. Chem. Soc.* 103: 3185-3191) or using automated synthesis methods. In addition, larger DNA segments can readily be prepared by well known methods, such as synthesis of a group of oligonucleotides that define various modular segments of the gene, followed by ligation of oligonucleotides to build the complete modified gene.

The nucleic acid molecules of the present invention may further be modified so as to contain a detectable label for diagnostic and probe purposes. A variety of such labels are known in the art and can readily be employed with the encoding molecules herein described. Suitable labels include, but are not limited to, biotin, radiolabeled or fluorescently labeled nucleotides and the like. A skilled artisan can readily employ any such label to obtain labeled variants of the nucleic acid molecules of the invention.

C. Isolation of Other Related Nucleic Acid Molecules

As described above, the identification and characterization of the nucleic acid molecule having SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 allows a skilled artisan to isolate nucleic acid molecules that encode other members of the protein family in addition to the sequences herein described. Further, the presently disclosed nucleic acid molecules allow a skilled artisan to isolate nucleic acid molecules that encode other members of the family of proteins in addition to the proteins having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

For instance, a skilled artisan can readily use the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 to generate antibody probes to screen expression libraries prepared from appropriate cells. Typically, polyclonal antiserum from mammals such as rabbits immunized with the purified protein (as described below) or monoclonal antibodies can be used to probe a mammalian cDNA or genomic expression library, such as lambda gtl1 library, to obtain the appropriate coding sequence for other members of the protein family. The cloned cDNA sequence can be expressed as a fusion protein,

expressed directly using its own control sequences, or expressed by constructions using control sequences appropriate to the particular host used for expression of the enzyme.

Alternatively, a portion of the coding sequence herein described can be synthesized and used as a probe to retrieve DNA encoding a member of the protein family from any mammalian organism. Oligomers containing approximately 18-20 nucleotides (encoding about a 6-7 amino acid stretch) are prepared and used to screen genomic DNA or cDNA libraries to obtain hybridization under stringent conditions or conditions of sufficient stringency to eliminate an undue level of false positives.

Additionally, pairs of oligonucleotide primers can be prepared for use in PCR to selectively clone an encoding nucleic acid molecule. A PCR denature/anneal/extend cycle for using such PCR primers is well known in the art and can readily be adapted for use in isolating other encoding nucleic acid molecules.

Nucleic acid molecules encoding other members of the protein family may also be identified in existing genomic or other sequence information using any available computational method, including but not limited to: PSI-BLAST (Altschul *et al.* (1997), *Nucl. Acids Res.* 25: 3389-3402); PHI-BLAST (Zhang *et al.* (1998), *Nucl. Acids Res.* 26: 3986-3990), 3D-PSSM (Kelly *et al.* (2000), *J. Mol. Biol.* 299: 499-520); and other computational analysis methods (Shi *et al.* (1999), *Biochem. Biophys. Res. Commun.* 262: 132-138 and Matsunami *et al.* (2000), *Nature* 404: 601-604).

20 D. rDNA molecules Containing a Nucleic Acid Molecule

The present invention further provides recombinant DNA molecules (rDNAs) that contain a coding sequence. As used herein, a rDNA molecule is a DNA molecule that has been subjected to molecular manipulation *in situ*. Methods for generating rDNA molecules are well known in the art, for example, see Sambrook *et al.*, Molecular Cloning- A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold

Spring Harbor, NY, 2001. In the preferred rDNA molecules, a coding DNA sequence is operably linked to expression control sequences and/or vector sequences.

5 The choice of vector and/or expression control sequences to which one of the protein family encoding sequences of the present invention is operably linked depends directly, as is well known in the art, on the functional properties desired, *e.g.*, protein expression, and the host cell to be transformed. A vector contemplated by the present invention is at least capable of directing the replication or insertion into the host chromosome, and preferably also expression, of the structural gene included in the rDNA molecule.

10 Expression control elements that are used for regulating the expression of an operably linked protein encoding sequence are known in the art and include, but are not limited to, inducible promoters, constitutive promoters, secretion signals, and other regulatory elements. Preferably, the inducible promoter is readily controlled, such as being responsive to a nutrient in the host cell's medium.

15 In one embodiment, the vector containing a coding nucleic acid molecule will include a prokaryotic replicon, *i.e.*, a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extrachromosomally in a prokaryotic host cell, such as a bacterial host cell, transformed therewith. Such replicons are well known in the art. In addition, vectors that include a
20 prokaryotic replicon may also include a gene whose expression confers a detectable marker such as a drug resistance. Typical bacterial drug resistance genes are those that confer resistance to ampicillin, kanamycin, chloramphenicol or tetracycline.

Vectors that include a prokaryotic replicon can further include a prokaryotic or bacteriophage promoter capable of directing the expression (transcription and translation)
25 of the coding gene sequences in a bacterial host cell, such as *E. coli*. A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with bacterial

hosts are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention. Typical of such vector plasmids are pUC8, pUC9, pBR322 and pBR329 available from BioRad Laboratories, (Richmond, CA), pPL and pKK223 available from Pharmacia (Piscataway, NJ).

5 Expression vectors compatible with eukaryotic cells, preferably those compatible with vertebrate cells, can also be used to form rDNA molecules that contain a coding sequence. Eukaryotic cell expression vectors, including viral vectors, are well known in the art and are available from several commercial sources. Typically, such vectors are provided containing convenient restriction sites for insertion of the desired DNA segment.

10 Typical of such vectors are pSVL and pKSV-10 (Pharmacia), pBPV-1/pML2d (International Biotechnologies, Inc.), pTDT1 (ATCC, #31255), the vector pCDM8 described herein, and the like eukaryotic expression vectors. Vectors may be modified to include tissue specific promoters if needed.

Eukaryotic cell expression vectors used to construct the rDNA molecules of the present invention may further include a selectable marker that is effective in an eukaryotic cell, preferably a drug resistance selection marker. A preferred drug resistance marker is the gene whose expression results in neomycin resistance, *i.e.*, the neomycin phosphotransferase (*neo*) gene. (Southern *et al.* (1982), *J. Mol. Anal. Genet.* 1:327-341). Alternatively, the selectable marker can be present on a separate plasmid, and the two

15 vectors are introduced by co-transfection of the host cell, and selected by culturing in the appropriate drug for the selectable marker.

20

E. Host Cells Containing an Exogenously Supplied Coding Nucleic Acid Molecule

The present invention further provides host cells transformed with a nucleic acid molecule that encodes a protein of the present invention. The host cell can be either

25 prokaryotic or eukaryotic. Eukaryotic cells useful for expression of a protein of the invention are not limited, so long as the cell line is compatible with cell culture methods

and compatible with the propagation of the expression vector and expression of the gene product. Preferred eukaryotic host cells include, but are not limited to, yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human cell line. Preferred eukaryotic host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells (NIH/3T3) available from the ATCC as CRL 1658, baby hamster kidney cells (BHK), and the like eukaryotic tissue culture cell lines.

Any prokaryotic host can be used to express a rDNA molecule encoding a protein of the invention. The preferred prokaryotic host is *E. coli*.

Transformation of appropriate cell hosts with a rDNA molecule of the present invention is accomplished by well known methods that typically depend on the type of vector used and host system employed. With regard to transformation of prokaryotic host cells, electroporation and salt treatment methods are typically employed (see, for example, Cohen *et al.* (1972), *Proc. Natl. Acad. Sci. USA* 69: 2110; and Sambrook *et al.*, *supra*). With regard to transformation of vertebrate cells with vectors containing rDNAs, electroporation, cationic lipid or salt treatment methods are typically employed, see, for example, Graham *et al.* (1973), *Viol.* 52: 456; Wigler *et al.* (1979), *Proc. Natl. Acad. Sci. USA* 76: 1373-1376.

Successfully transformed cells, *i.e.*, cells that contain a rDNA molecule of the present invention, can be identified by well known techniques including the selection for a selectable marker. For example, cells resulting from the introduction of an rDNA of the present invention can be cloned to produce single colonies. Cells from those colonies can be harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, (1975) *J. Mol. Biol.* 98: 503 or Berent *et al.*, (1985) *Biotech.* 3: 208, or the proteins produced from the cell assayed via an immunological method.

F. Production of Recombinant Proteins using a rDNA Molecule

The present invention further provides methods for producing a protein of the invention using nucleic acid molecules herein described. In general terms, the production of a recombinant form of a protein typically involves the following steps:

5 First, a nucleic acid molecule is obtained that encodes a protein of the invention, such as a nucleic acid molecule comprising, consisting essentially of or consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, or nucleotides 390-4883 or 390-4880 of SEQ ID NO: 1, or nucleotides 12-4907 or 12-4904 of SEQ ID NO: 3, or nucleotides 424-1911 or 424-1908 of SEQ ID NO: 5, or nucleotides 405-1838 or 405-1835 of SEQ ID NO: 7, or
10 nucleotides 89-1153 or 89-1150 of SEQ ID NO: 9, or nucleotides 223-1572 or 223-1569 of SEQ ID NO: 11, or 418-1395 or 418-1392 of SEQ ID NO: 13, or nucleotides 271-1434 or 271-1431 of SEQ ID NO: 15. If the encoding sequence is uninterrupted by introns, as are these open-reading-frames, it is directly suitable for expression in any host.

The nucleic acid molecule is then preferably placed in operable linkage with
15 suitable control sequences, as described above, to form an expression unit containing the protein open reading frame. The expression unit is used to transform a suitable host and the transformed host is cultured under conditions that allow the production of the recombinant protein. Optionally the recombinant protein is isolated from the medium or from the cells; recovery and purification of the protein may not be necessary in some
20 instances where some impurities may be tolerated.

Each of the foregoing steps can be done in a variety of ways. For example, the desired coding sequences may be obtained from genomic fragments and used directly in appropriate hosts. The construction of expression vectors that are operable in a variety of hosts is accomplished using appropriate replicons and control sequences, as set forth
25 above. The control sequences, expression vectors, and transformation methods are dependent on the type of host cell used to express the gene and were discussed in detail earlier. Suitable restriction sites can, if not normally available, be added to the ends of the

coding sequence so as to provide an excisable gene to insert into these vectors. A skilled artisan can readily adapt any host/expression system known in the art for use with the nucleic acid molecules of the invention to produce recombinant protein.

G. Methods to Identify Agents that Modulate the Expression of a Nucleic Acid

5 Encoding the Genes Associated with Cancer

Another embodiment of the present invention provides methods for identifying agents that modulate the expression of a nucleic acid encoding a protein of the invention such as a protein having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Such assays may utilize any available means of monitoring for changes in the
10 expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, cell lines that contain reporter gene fusions between nucleotides from within the open reading frame defined by nucleotides 390-4883 of SEQ
15 ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1911 of SEQ ID NO: 5, nucleotides 405-1838 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1572 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, nucleotides 271-1434 of SEQ ID NO: 15, and/or the 5' and/or 3' regulatory elements and any assayable fusion partner may be prepared. Numerous assayable fusion partners are
20 known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990), *Anal. Biochem.* 188: 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which
25 modulate the expression of a nucleic acid of the invention.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a nucleic acid encoding a protein of the invention, such as the protein having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. For instance, mRNA expression may be monitored directly by hybridization to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, Molecular Cloning - A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001.

The preferred cells will be those derived from human tissue, for instance, biopsy tissue or cultured cells from patients with cancer. Cell lines such as ATCC breast ductal carcinoma cell lines (Catalogue Nos. CRL-2320, CRL-2338, and CRL-7345), ATCC colorectal adenocarcinoma cell lines (Catalogue Nos. CCL-222, CCL-224, CCL-225, CCL-234, CRL-7159, and CRL-7184), ATCC kidney clear cell carcinoma cell lines (Catalogue Nos. HTB-46 and HTB-47), ATCC renal cell adenocarcinoma cell lines (Catalogue Nos. CRL-1611, CRL-1932 and CRL-1933), ATCC liver hepatocellular carcinoma cell lines (Catalogue Nos. CRL-2233, CRL-2234, and HB-8065), ATCC lung adenocarcinoma cell lines (Catalogue Nos. CRL-5944, CRL-7380, and CRL-5907), ATCC lymphoma cell lines (Catalogue Nos. CRL-7936, CRL-7264, and CRL-7507), ATCC ovary adenocarcinoma cell lines (Catalogue Nos. HTB-161, HTB-75, and HTB-76), ATCC pancreas adenocarcinoma cell lines (Catalogue Nos. CRL-1687, CRL-2119, and HTP-79), prostate adenocarcinoma cell lines (Catalogue Nos. CRL-1435, CRL-2422, and CRL-2220), and ATCC gastric adenocarcinoma cell lines (Catalogue Nos. CRL-1739, CRL-1863, and CRL-1864) may be used. Alternatively, other available cells or cell lines may be used.

Probes to detect differences in RNA expression levels between cells exposed to the agent and control cells may be prepared from the nucleic acids of the invention. It is preferable, but not necessary, to design probes which hybridize only with target nucleic acids under conditions of high stringency. Only highly complementary nucleic acid

hybrids form under conditions of high stringency. Accordingly, the stringency of the assay conditions determines the amount of complementarity which should exist between two nucleic acid strands in order to form a hybrid. Stringency should be chosen to maximize the difference in stability between the probe:target hybrid and probe:non-target hybrids.

Probes may be designed from the nucleic acids of the invention through methods known in the art. For instance, the G+C content of the probe and the probe length can affect probe binding to its target sequence. Methods to optimize probe specificity are commonly available in Sambrook *et al.*, *supra*, or Ausubel *et al.*, Short Protocols in Molecular Biology, Fourth Ed., John Wiley & Sons, Inc., New York, 1999.

Hybridization conditions are modified using known methods, such as those described by Sambrook *et al.* and Ausubel *et al.* as required for each probe. Hybridization of total cellular RNA or RNA enriched for polyA RNA can be accomplished in any available format. For instance, total cellular RNA or RNA enriched for polyA RNA can be affixed to a solid support and the solid support exposed to at least one probe comprising at least one, or part of one of the sequences of the invention under conditions in which the probe will specifically hybridize. Alternatively, nucleic acid fragments comprising at least one, or part of one of the sequences of the invention can be affixed to a solid support, such as a silicon chip, porous glass wafer or membrane. The solid support can then be exposed to total cellular RNA or polyA RNA from a sample under conditions in which the affixed sequences will specifically hybridize. Such solid supports and hybridization methods are widely available, for example, those disclosed by Beattie, (1995) WO 95/11755. By examining for the ability of a given probe to specifically hybridize to an RNA sample from an untreated cell population and from a cell population exposed to the agent, agents which up- or down-regulate the expression of a nucleic acid encoding the protein having the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 are identified.

Hybridization for qualitative and quantitative analysis of mRNAs may also be carried out by using a RNase Protection Assay (*i.e.*, RPA, see Ma *et al.* (1996), *Methods* 10: 273-238). Briefly, an expression vehicle comprising cDNA encoding the gene product and a phage specific DNA dependent RNA polymerase promoter (*e.g.*, T7, T3 or SP6 RNA polymerase) is linearized at the 3' end of the cDNA molecule, downstream from the phage promoter, wherein such a linearized molecule is subsequently used as a template for synthesis of a labeled antisense transcript of the cDNA by *in vitro* transcription. The labeled transcript is then hybridized to a mixture of isolated RNA (*i.e.*, total or fractionated mRNA) by incubation at 45°C overnight in a buffer comprising 80% formamide, 40 mM Pipes, pH 6.4, 0.4 M NaCl and 1 mM EDTA. The resulting hybrids are then digested in a buffer comprising 40 µg/ml ribonuclease A and 2 µg/ml ribonuclease. After deactivation and extraction of extraneous proteins, the samples are loaded onto urea/polyacrylamide gels for analysis.

In another assay, to identify agents which affect the expression of the instant gene products, cells or cell lines are first identified which express the gene products of the invention physiologically. Cells and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines would be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5' promoter-containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag or other detectable marker. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions. For example, the agent in a pharmaceutically acceptable excipient is contacted with cells in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the “agent-contacted” sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the “agent-contacted” sample compared to the control will be used to distinguish the effectiveness of the agent.

H. Methods to Identify Agents that Modulate the Level or at Least One Activity of the Cancer Associated Proteins

Another embodiment of the present invention provides methods for identifying agents that modulate the level or at least one activity of a protein of the invention such as the protein having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Such methods or assays may utilize any means of monitoring or detecting the desired activity and are particularly useful for identifying agents that treat cancer.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell

line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe.

Antibody probes are prepared by immunizing suitable mammalian hosts in appropriate immunization protocols using the peptides, polypeptides or proteins of the invention if they are of sufficient length, or, if desired, or if required to enhance immunogenicity, conjugated to suitable carriers. Methods for preparing immunogenic conjugates with carriers such as BSA, KLH, or other carrier proteins are well known in the art. In some circumstances, direct conjugation using, for example, carbodiimide reagents may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co. (Rockford, IL), may be desirable to provide accessibility to the hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues, for example, to facilitate linking to a carrier. Administration of the immunogens is conducted generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation.

While the polyclonal antisera produced in this way may be satisfactory for some applications, for pharmaceutical compositions, use of monoclonal preparations is preferred. Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using the standard method of Kohler and Milstein ((1975) *Nature* 256: 495-497) or modifications which effect immortalization of lymphocytes or spleen cells, as is generally known. The immortalized cell lines secreting the desired antibodies are screened by immunoassay in which the antigen is the peptide hapten, polypeptide or protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid.

The desired monoclonal antibodies are then recovered from the culture supernatant or from the ascites supernatant. Fragments of the monoclonal antibodies or the polyclonal

antisera which contain the immunologically significant (antigen-binding) portion can be used as antagonists, as well as the intact antibodies. Use of immunologically reactive (antigen-binding) antibody fragments, such as the Fab, Fab', or F(ab')₂ fragments is often preferable, especially in a therapeutic context, as these fragments are generally less immunogenic than the whole immunoglobulin.

The antibodies or antigen-binding fragments may also be produced, using current technology, by recombinant means. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras with multiple species origin, such as humanized antibodies.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and

functionally similar to the parent peptide (see Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, Inc., New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

5 The peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production using solid phase peptide synthesis is necessitated if
10 non-gene-encoded amino acids are to be included.

 Another class of agents of the present invention are antibodies immunoreactive with critical positions of proteins of the invention, e.g., cytoplasmic domain, spacer domain, α -helical coiled-coil domain, or the receptor domain, as described herein. Antibody agents are obtained by immunization of suitable mammalian subjects with
15 peptides, containing as antigenic regions, those portions of the protein intended to be targeted by the antibodies.

I. Uses for Agents that Modulate the Expression or at Least one Activity of the Proteins Associated with Cancer

 As provided in the Examples, the proteins and nucleic acids of the invention, such
20 as the proteins having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, are differentially expressed in cancerous tissue. Agents that up- or down- regulate or modulate the expression of the protein or at least one activity of the protein, such as agonists or antagonists, may be used to modulate biological and pathologic processes associated with the protein's function and activity. This includes agents identified
25 employing homologues and analogues of the present invention.

As used herein, a subject can be any mammal, so long as the mammal is in need of modulation of a pathological or biological process mediated by a protein of the invention. The term "mammal" is defined as an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects.

5 Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression of a protein of the invention may be associated with cell growth or hyperplasia. As used herein, an agent is said to modulate a pathological process when the agent reduces the degree or severity of the process. For instance, cancer may be prevented or disease progression modulated by the administration
10 of agents which up- or down-regulate or modulate in some way the expression or at least one activity of a protein of the invention.

The agents of the present invention can be provided alone, or in combination with other agents that modulate a particular pathological process. For example, an agent of the present invention can be administered in combination with other known drugs. As used
15 herein, two agents are said to be administered in combination when the two agents are administered simultaneously or are administered independently in a fashion such that the agents will act at the same time.

The agents of the present invention can be administered via parenteral, subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, or buccal routes.
20 Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

The present invention further provides compositions containing one or more agents which modulate expression or at least one activity of a protein of the invention. While
25 individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 0.1 to 100 µg/kg body

wt. The preferred dosages comprise 0.1 to 10 $\mu\text{g/kg}$ body wt. The most preferred dosages comprise 0.1 to 1 $\mu\text{g/kg}$ body wt.

In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients
5 and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be
10 administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers. Liposomes can also be used to
15 encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic administration of the active ingredient.

20 Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In practicing the methods of this invention, the compounds of this invention may be used alone or in combination, or in combination with other therapeutic or diagnostic
25 agents. In certain preferred embodiments, the compounds of this invention may be coadministered along with other compounds typically prescribed for these conditions according to generally accepted medical practice. The compounds of this invention can be

utilized *in vivo*, ordinarily in mammals, such as humans, sheep, horses, cattle, pigs, dogs, cats, rats and mice, or *in vitro*.

J. Methods to Identify Binding Partners

Another embodiment of the present invention provides methods for isolating and
5 identifying binding partners of proteins of the invention. In general, a protein of the
invention is mixed with a potential binding partner or an extract or fraction of a cell under
conditions that allow the association of potential binding partners with the protein of the
invention. After mixing, peptides, polypeptides, proteins or other molecules that have
become associated with a protein of the invention are separated from the mixture. The
10 binding partner that bound to the protein of the invention can then be removed and further
analyzed. To identify and isolate a binding partner, the entire protein, for instance a
protein comprising the entire amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or
16 can be used. Alternatively, a fragment of the protein can be used.

As used herein, a cellular extract refers to a preparation or fraction which is made
15 from a lysed or disrupted cell. The preferred source of cellular extracts will be cells
derived from human tumors or transformed cells, for instance, biopsy tissue or tissue
culture cells from carcinomas. Alternatively, cellular extracts may be prepared from
normal tissue or available cell lines.

A variety of methods can be used to obtain an extract of a cell. Cells can be
20 disrupted using either physical or chemical disruption methods. Examples of physical
disruption methods include, but are not limited to, sonication and mechanical shearing.
Examples of chemical lysis methods include, but are not limited to, detergent lysis and
enzyme lysis. A skilled artisan can readily adapt methods for preparing cellular extracts in
order to obtain extracts for use in the present methods.

25 Once an extract of a cell is prepared, the extract is mixed with the protein of the
invention under conditions in which association of the protein with the binding partner can

occur. A variety of conditions can be used, the most preferred being conditions that closely resemble conditions found in the cytoplasm of a human cell. Features such as osmolarity, pH, temperature, and the concentration of cellular extract used, can be varied to optimize the association of the protein with the binding partner.

5 After mixing under appropriate conditions, the bound complex is separated from the mixture. A variety of techniques can be utilized to separate the mixture. For example, antibodies specific to a protein of the invention can be used to immunoprecipitate the binding partner complex. Alternatively, standard chemical separation techniques such as chromatography and density/sediment centrifugation can be used.

10 After removal of non-associated cellular constituents found in the extract, the binding partner can be dissociated from the complex using conventional methods. For example, dissociation can be accomplished by altering the salt concentration or pH of the mixture.

 To aid in separating associated binding partner pairs from the mixed extract, the
15 protein of the invention can be immobilized on a solid support. For example, the protein can be attached to a nitrocellulose matrix or acrylic beads. Attachment of the protein to a solid support aids in separating peptide/binding partner pairs from other constituents found in the extract. The identified binding partners can be either a single protein or a complex made up of two or more proteins. Alternatively, binding partners may be identified using
20 a Far-Western assay according to the procedures of Takayama *et al.* (1997), *Methods Mol. Biol.* 69: 171-184 or Sauder *et al.* (1996), *J. Gen. Virol.* 77: 991-996 or identified through the use of epitope tagged proteins or GST fusion proteins.

 Alternatively, the nucleic acid molecules of the invention can be used in a yeast
two-hybrid system or other *in vivo* protein-protein detection system. The yeast two-hybrid
25 system has been used to identify other protein partner pairs and can readily be adapted to employ the nucleic acid molecules herein described.

K. Use of the Binding Partners of the Cancer Associated Proteins

Once isolated, the binding partners of the proteins of the invention, and homologues and analogues thereof, obtained using the above described methods can be used for a variety of purposes. The binding partners can be used to generate antibodies
5 that bind to the binding partner using techniques known in the art. Antibodies that bind the binding partner can be used to assay the activity of the protein of the invention, as a therapeutic agent to modulate a biological or pathological process mediated by the protein of the invention, or to purify the binding partner. These uses are described in detail below.

L. Methods to Identify Agents that Block the Associations between the Binding 10 Partners and the Cancer Associated Proteins

Another embodiment of the present invention provides methods for identifying agents that reduce or block the association of a protein of the invention with a binding partner. Specifically, a protein of the invention is mixed with a binding partner in the presence and absence of an agent to be tested. After mixing under conditions that allow
15 association of the proteins, the two mixtures are analyzed and compared to determine if the agent reduced or blocked the association of the protein of the invention with the binding partner. Agents that block or reduce the association of the protein of the invention with the binding partner will be identified as decreasing the amount of association present in the sample containing the tested agent.

20 As used herein, an agent is said to reduce or block the association between a protein of the invention and a binding partner when the presence of the agent decreases the extent to which or prevents the binding partner from becoming associated with the protein of the invention. One class of agents will reduce or block the association by binding to the binding partner while another class of agents will reduce or block the association by
25 binding to the protein of the invention.

The binding partner used in the above assay can either be an isolated and fully characterized protein or can be a partially characterized protein that binds to the protein of the invention or a binding partner that has been identified as being present in a cellular extract. It will be apparent to one of ordinary skill in the art that so long as the binding partner has been characterized by an identifiable property, e.g., molecular weight, the present assay can be used.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the protein of the invention with the binding partner. An example of randomly selected agents is the use of a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up the contact sites of the binding partner with the protein of the invention. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to the contact site of the protein of the invention on the binding partner. Such an agent will reduce or block the association of the protein of the invention with the binding partner by binding to the binding partner.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

One class of agents of the present invention are peptide agents whose amino acid sequences are chosen based on the amino acid sequence of the protein of the invention. The peptide agents of the invention can be prepared using standard solid phase (or

solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production using solid phase peptide synthesis is necessitated if
5 non-gene encoded amino acids are to be included.

Another class of agents of the present invention are antibodies immunoreactive with critical positions of the protein of the invention or the binding partner. As described above, antibodies are obtained by immunization of suitable mammalian subjects with peptides, containing as antigenic regions, those portions of the protein of the invention or
10 the binding partner, intended to be targeted by the antibodies. Critical regions include the contact sites involved in the association of the protein of the invention with the binding partner.

As discussed below, the important minimal sequence of residues involved in activity of the protein of the invention define a functional linear domain that can be
15 effectively used as a bait for two hybrid screening and identification of potential associated molecules. Use of such fragments will significantly increase the specificity of the screening as opposed to using the full-length molecule and is therefore preferred. Similarly, this linear sequence can be also used as an affinity matrix also to isolate binding proteins using a biochemical affinity purification strategy.

20 **M. Uses for Agents that Block the Associations between the Binding Partners and the Cancer Associated Proteins**

As provided in the Examples, the proteins and nucleic acids of the invention, such as the proteins having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, are differentially expressed in cancerous tissue. Agents that reduce or block the
25 interactions of a protein of the invention, including those identified employing

homologues and analogues of the protein, with a binding partner may be used to modulate biological and pathologic processes associated with the protein's function and activity.

As used herein, a subject can be any mammal, so long as the mammal is in need of modulation of a pathological or biological process mediated by a protein of the invention.

5 The term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects.

Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression of a protein of the invention may be associated with cell growth or hyperplasia. As used herein, an agent is said to modulate a pathological process when the agent reduces the degree or severity of the process. For instance, cancer may be prevented or disease progression modulated by the administration of agents that reduce or block the interactions of a protein of the invention with a binding partner.

15 The agents of the present invention can be administered via parenteral, subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

20 The present invention further provides compositions containing one or more agents that block association of a protein of the invention with a binding partner. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 0.1 to 100 $\mu\text{g/kg}$ body wt. The preferred dosages comprise 0.1 to 10 $\mu\text{g/kg}$ body wt. The most preferred dosages comprise 0.1 to 1 $\mu\text{g/kg}$ body wt.

25 In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients

and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water soluble form, for example, water soluble salts. In addition, 5 suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. 10 Optionally, the suspension may also contain stabilizers. Liposomes can also be used to encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic 15 administration of the active ingredient.

Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In practicing the methods of this invention, the compounds of this invention may 20 be used alone or in combination, or in combination with other therapeutic or diagnostic agents. In certain preferred embodiments, the compounds of this invention may be coadministered along with other compounds typically prescribed for these conditions according to generally accepted medical practice. The compounds of this invention can be utilized *in vivo*, ordinarily in mammals, such as humans, sheep, horses, cattle, pigs, dogs, 25 cats, rats and mice, or *in vitro*.

N. Rational Drug Design and Combinatorial Chemistry

The present invention further encompasses rational drug design and combinatorial chemistry. Those of skill will recognize appropriate methods to utilize and exploit aspects of the present invention in identifying compounds which can be developed for cancer treatment. Rational drug design involving polypeptides requires identifying and defining
5 a first peptide with which the designed drug is to interact, and using the first target peptide to define the requirements for a second peptide. With such requirements defined, one can find or prepare an appropriate peptide or non-peptide that meets all or substantially all of the defined requirements. Thus, one goal of rational drug design is to produce structural or functional analogs of biologically active polypeptides of interest or of small molecules
10 with which they interact (e.g., agonists, antagonists, null compounds) in order to fashion drugs that are, for example, more or less potent forms of the ligand. (See, e.g., Hodgson (1991), *Bio. Technology* 9:19-21). Combinatorial chemistry is the science of synthesizing and testing compounds for bioactivity en masse, instead of one by one, the aim being to discover drugs and materials more quickly and inexpensively than was formerly possible.
15 Rational drug design and combinatorial chemistry have become more intimately related in recent years due to the development of approaches in computer-aided protein modeling and drug discovery. (See e.g., US Pat. No. 4,908,773; 5,884,230; 5,873,052; 5,331,573; and 5,888,738).

The use of molecular modeling as a tool for rational drug design and combinatorial
20 chemistry has dramatically increased due to the advent of computer graphics. Not only is it possible to view molecules on computer screens in three dimensions but it is also possible to examine the interactions of macromolecules such as enzymes and receptors and rationally designed derivative molecules to test. (See Boorman (1992), *Chem. Eng. News* 70:18-26). A vast amount of user-friendly software and hardware is now available
25 and virtually all pharmaceutical companies have computer modeling groups devoted to rational drug design. Molecular Simulations Inc. (www.msi.com), for example, sells several sophisticated programs that allow a user to start from an amino acid sequence, build a two or three-dimensional model of the protein or polypeptide, compare it to other

two and three-dimensional models, and analyze the interactions of compounds, drugs, and peptides with a three dimensional model in real time. Accordingly, in some embodiments of the invention, software is used to compare regions of the invention protein and molecules that interact therewith (collectively referred to as "binding partners" --e.g., anti-
5 protein antibodies), and fragments or derivatives of these molecules with other molecules, such as peptides, peptidomimetics, and chemicals, so that therapeutic interactions can be predicted and designed. (See Schneider (1998), *Genetic Engineering News* December: page 20; Tempczyk *et al.* (1997), Molecular Simulations Inc. Solutions April; and Butenhof (1998), Molecular Simulations Inc. Case Notes (August 1998) for a discussion
10 of molecular modeling).

O. Gene Therapy

In another embodiment, genetic therapy can be used as a means for modulating biological and pathologic processes associated with the protein's function and activity. This comprises inserting into a cancerous cell a gene construct encoding a protein
15 comprising all or at least a portion of the sequences of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, or alternatively a gene construct comprising all or a portion of the non-coding region of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, operably linked to a promoter or enhancer element such that expression of said protein causes suppression of said cancer and wherein said promoter or enhancer element is a promoter or enhancer element
20 modulating said gene construct.

In the constructs described, expression of said protein can be directed from any suitable promoter (e.g., the human cytomegalovirus (CMV), simian virus 40 (SV40), or metallothionein promoters), and regulated by any appropriate mammalian regulatory element. For example, if desired, enhancers known to preferentially direct gene expression
25 in neural cells, T cells, or B cells may be used to direct the expression. The enhancers used could include, without limitation, those that are characterized as tissue or cell specific in their expression. Alternatively, if a genomic clone of LFG1, LFG2, LFG3, LFG4, LFG5

or LFG6 is used as a therapeutic construct (for example, following its isolation by hybridization with the nucleic acid molecule of the invention described above), regulation may be mediated by the cognate regulatory sequences or, if desired, by regulatory sequences derived from a heterologous source, including any of the promoters or regulatory elements described above.

Insertion of the construct into a cancerous cell is accomplished *in vivo*, for example using a viral or plasmid vector. Such methods can also be applied to *in vitro* uses. Thus, the methods of the present invention are readily applicable to different forms of gene therapy, either where cells are genetically modified *ex vivo* and then administered to a host or where the gene modification is conducted *in vivo* using any of a number of suitable methods involving vectors especially suitable to such therapies.

Retroviral vectors, adenoviral vectors, adeno-associated viral vectors, or other viral vectors with the appropriate tropism for cells likely to be involved in cancer (for example, epithelial cells) may be used as a gene transfer delivery system for a therapeutic gene construct. Numerous vectors useful for this purpose are generally known (Cozzi PJ, et al., (2002) *Prostate*, 53(2):95-100; Bitzer M, Lauer U., (2002) *Dtsch Med Wochenschr.* 127(31-32):1623-1624; Mezzina and Danos (2002), *Trends Genet.* 8:241-256; Loser et al. (2002) *Curr. Gene Ther.* 2:161-171; Pfeifer and Verma (2001), *Annu. Rev. Genomics Hum. Genet.* 2:177-211). Retroviral vectors are particularly well developed and have been used in clinical settings (Anderson et al. (1995), U.S. Patent No. 5,399,346). Non-viral approaches may also be employed for the introduction of therapeutic DNA into cells otherwise predicted to undergo cancer (Jeschke et al. (20002) *Curr. Gene Ther.* 1:267-278; Wu et al. (1988), *J. Biol. Chem.* 263:14621-14624; Wu et al. (1989), *J. Biol. Chem.* 264:16985-16987). For example, a gene may be introduced into a neuron or a T cell by lipofection, asialorosanucoid polylysine conjugation, or, less preferably, microinjection under surgical conditions.

For any of the methods of application described above, the therapeutic nucleic acid construct is preferably applied to the site of the cancer event (for example, by injection). However, it may also be applied to tissue in the vicinity of the cancer event or to a blood vessel supplying the cells predicted to undergo cancer.

5 P. Transgenic Animals

Transgenic animals containing mutant, knock-out or modified genes corresponding to the cDNA sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, or the open reading frame encoding the polypeptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, or fragments thereof having a consecutive sequence of at least about 3, 4, 5, 6, 10, 15, 20, 25,
10 30, 35 or more amino acid residues, are also included in the invention. Transgenic animals are genetically modified animals into which recombinant, exogenous or cloned genetic material has been experimentally transferred. Such genetic material is often referred to as a "transgene." The nucleic acid sequence of the transgene, in this case a form of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, may be integrated either at a locus of a
15 genome where that particular nucleic acid sequence is not otherwise normally found or at the normal locus for the transgene. The transgene may consist of nucleic acid sequences derived from the genome of the same species or of a different species than the species of the target animal.

In some embodiments, transgenic animals in which all or a portion of a gene
20 comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 is deleted may be constructed. In those cases where the gene corresponding to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 contains one or more introns, the entire gene- all exons, introns and the regulatory sequences- may be deleted. Alternatively, less than the entire gene may be deleted. For example, a single exon and/or intron may be deleted, so as to create an animal expressing a modified version
25 of a protein of the invention.

The term "germ cell line transgenic animal" refers to a transgenic animal in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring the ability of the transgenic animal to transfer the genetic information to offspring. If such offspring in fact possess some or all of that alteration or genetic information, then they too are transgenic animals.

The alteration or genetic information may be foreign to the species of animal to which the recipient belongs, foreign only to the particular individual recipient, or may be genetic information already possessed by the recipient. In the last case, the altered or introduced gene may be expressed differently than the native gene.

Transgenic animals can be produced by a variety of different methods including transfection, electroporation, microinjection, gene targeting in embryonic stem cells and recombinant viral and retroviral infection (*see, e.g.*, U.S. Patent No. 4,736,866; U.S. Patent No. 5,602,307; Mullins *et al.* (1993), *Hypertension* 22: 630-633; Brenin *et al.* (1997), *Surg. Oncol.* 6: 99-110; Recombinant Gene Expression Protocols (Methods in Molecular Biology, Vol. 62), Tuan, ed., Humana Press, Totowa, NJ, 1997).

A number of recombinant or transgenic mice have been produced, including those which express an activated oncogene sequence (U.S. Patent No. 4,736,866); express simian SV40 T-antigen (U.S. Patent No. 5,728,915); lack the expression of interferon regulatory factor 1 (IRF-1) (U.S. Patent No. 5,731,490); exhibit dopaminergic dysfunction (U.S. Patent No. 5,723,719); express at least one human gene which participates in blood pressure control (U.S. Patent No. 5,731,489); display greater similarity to the conditions existing in naturally occurring Alzheimer's disease (U.S. Patent No. 5,720,936); have a reduced capacity to mediate cellular adhesion (U.S. Patent No. 5,602,307); possess a bovine growth hormone gene (Clutter *et al.* (1996), *Genetics* 143: 1753-1760); or, are capable of generating a fully human antibody response (McCarthy (1997), *Lancet* 349: 405).

While mice and rats remain the animals of choice for most transgenic experimentation, in some instances it is preferable or even necessary to use alternative animal species. Transgenic procedures have been successfully utilized in a variety of non-murine animals, including sheep, goats, pigs, dogs, cats, monkeys, chimpanzees, hamsters, rabbits, cows and guinea pigs (see, *e.g.*, Kim *et al.* (1997), *Mol. Reprod. Dev.* 46: 515-526; Houdebine (1995), *Reprod. Nutr. Dev.* 35: 609-617; Petters (1994), *Reprod. Fertil. Dev.* 6: 643-645; Schnieke *et al.* (1997), *Science* 278: 2130-2133; and Amoah (1997), *J. Animal Sci.* 75: 578-585).

The method of introduction of nucleic acid fragments into recombination competent mammalian cells can be by any method which favors co-transformation of multiple nucleic acid molecules. Detailed procedures for producing transgenic animals are readily available to one skilled in the art, including the disclosures in U.S. Patent No. 5,489,743 and U.S. Patent No. 5,602,307.

Q. Diagnostic Methods

As the genes and proteins of the invention are differentially expressed in cancerous tissues compared to non-cancerous tissues, the genes and proteins of the invention may be used to diagnose or monitor cancer, to track disease progression, or to differentiate cancerous tissue from non-cancerous tissue samples. One means of diagnosing cancer using the nucleic acid molecules or proteins of the invention involves obtaining tissue from living subjects.

Assays to detect nucleic acid or protein molecules of the invention may be in any available format. Typical assays for nucleic acid molecules include hybridization or PCR based formats. Typical assays for the detection of proteins, polypeptides or peptides of the invention include the use of antibody probes in any available format such as *in situ* binding assays, etc. (see Harlow & Lane, Antibodies - A Laboratory Manual, Cold Spring

Harbor Laboratory Press, Cold Spring Harbor, NY, 1988). In preferred embodiments, assays are carried-out with appropriate controls.

Generally, the diagnostics of the invention can be classified according to whether the embodiment is a nucleic acid or protein-based assay. Some diagnostic assays detect mutations or polymorphisms in the invention nucleic acids or proteins, which contribute to cancerous aberrations. Other diagnostic assays identify and distinguish defects in protein activity by detecting a level of invention RNA or protein in a tested organism that resembles the level of invention RNA or protein in a organism suffering from a disease, such as cancer, or by detecting a level of RNA or protein in a tested organism that is different than an organism not suffering from a disease.

Additionally, the manufacture of kits that incorporate the reagents and methods described in the following embodiments so as to allow for the rapid detection and identification of aberrations in protein activity or level are contemplated. The diagnostic kits can include a nucleic acid probe or an antibody or combinations thereof, which specifically detect a mutant form of the invention protein or a nucleic acid probe or an antibody or combinations thereof, which can be used to determine the level of RNA or protein expression of one or more invention protein. The detection component of these kits will typically be supplied in combination with one or more of the following reagents. A support capable of absorbing or otherwise binding DNA, RNA, or protein will often be supplied. Available supports include membranes of nitrocellulose, nylon or derivatized nylon that can be characterized by bearing an array of positively charged substituents. One or more restriction enzymes, control reagents, buffers, amplification enzymes, and non-human polynucleotides like calf-thymus or salmon-sperm DNA can be supplied in these kits.

Useful nucleic acid-based diagnostic techniques include, but are not limited to, direct DNA sequencing, gradient gel electrophoresis, Southern Blot analysis, single-stranded confirmation analysis (SSCA), RNase protection assay, dot blot analysis, nucleic

acid amplification, allele-specific PCR and combinations of these approaches. The starting point for these analyses is isolated or purified nucleic acid from a biological sample. It is contemplated that tissue biopsies would provide a good sample source. The nucleic acid is extracted from the sample and can be amplified by a DNA amplification technique such as the Polymerase Chain Reaction (PCR) using primers. Those of skill in the art will readily recognize methods available for confirming the presence of polymorphisms. In addition, any addressable array technology known in the art can be employed with this aspect of the invention. One particular embodiment of polynucleotide arrays is known as Genechips™, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092.

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid assays. There are several ways to produce labeled nucleic acids for hybridization or PCR including, but not limited to, oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, a nucleic acid encoding an invention protein can be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3 or SP6 and labeled nucleotides. A number of companies such as Pharmacia Biotech (Piscataway, NJ), Promega (Madison, WI), and U.S. Biochemical Corp (Cleveland, OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as, substrates, cofactors, inhibitors, magnetic particles and the like.

In preferred protein-based diagnostic, antibodies of the invention are attached to a support in an ordered array wherein a plurality of antibodies are attached to distinct regions of the support that do not overlap with each other. Those of skill in the art will readily recognize available assays that are protein-based diagnostics. Proteins are obtained from biological samples and are labeled by conventional approaches (e.g.,

radioactivity, colorimetrically, or fluorescently). Employing labeled standards of a known concentration of mutant and/or wild-type invention protein, an investigator can accurately determine the concentration of the invention protein in a sample and from this information can assess the expression level of the particular form of the protein. Conventional methods
5 in densitometry can also be used to more accurately determine the concentration or expression level of such protein. These approaches are also easily automated using technology known to those of skill in the art of high throughput diagnostic analysis. As detailed above, any addressable array technology known in the art can be employed with this aspect of the invention and display the protein arrays on the chips in an attempt to
10 maximize antibody binding patterns and diagnostic information.

As discussed above, the presence or detection of a polymorphism in an invention gene or protein can provide a diagnosis of a cancer or similar malady in an organism. Additional embodiments include the preparation of diagnostic kits comprising detection components, such as antibodies, specific for a particular polymorphic variant of invention
15 gene or protein. The detection component will typically be supplied in combination with one or more of the following reagents. A support capable of absorbing or otherwise binding RNA or protein will often be supplied. Available supports for this purpose include, but are not limited to, membranes of nitrocellulose, nylon or derivatized nylon that can be characterized by bearing an array of positively charged substituents, and Genechips™ or
20 their equivalents. One or more enzymes, such as Reverse Transcriptase and/or Taq polymerase, can be furnished in the kit, as can dNTPs, buffers, or non-human polynucleotides like calf-thymus or salmon-sperm DNA. Results from the kit assays can be interpreted by a healthcare provider or a diagnostic laboratory. Alternatively, diagnostic kits are manufactured and sold to private individuals for self-diagnosis.

25 In addition to diagnosing disease according to the presence or absence of a polymorphism, some diseases involving cancer result from skewed levels of invention protein or gene in particular tissues or aberrant patterns of invention protein expression. By monitoring the level of expression in various tissues, for example, a diagnosis can be

made or a disease state can be identified. Similarly, by determining ratios of the level of expression of various invention proteins in specific tissues (e.g., patterns of expression) a prognosis of health or disease can be made. The levels of invention protein expression in various tissues from healthy individuals, as well as, individuals suffering from cancers is
5 determined. These values can be recorded in a database and can be compared to values obtained from tested individuals. Additionally, the ratios or patterns of expression in various tissues from both healthy and diseased individuals is recorded in a database. These analyses are referred to as "disease state profiles" and by comparing one disease state profile (e.g. from a healthy or diseased individual) to a disease state profile from a tested
10 individual, a clinician can rapidly diagnose the presence or absence of disease.

The nucleic acid and protein-based diagnostic techniques described above can be used to detect the level or amount or ratio of expression of invention genes or proteins in a tissue. Through quantitative Northern hybridizations, *in situ* analysis, immunohistochemistry, ELISA, genechip array technology, PCR, and Western blots, for
15 example, the amount or level of expression of RNA or protein for a particular invention protein (wild-type or mutant) can be rapidly determined and from this information ratios of expression can be ascertained. Alternatively, the invention proteins to be analyzed can be family members that are currently unknown but which are identified based on their possession of one or more of the homology regions described above.

20 Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the
25 disclosure.

EXAMPLES

EXAMPLE 1: Identification of Differentially Expressed mRNA in Cancers - 1

Global changes in gene expression between tumor biopsies and normal tissues have been examined using the GeneExpress Oncology Datasuite™ of Gene Logic, Inc. (Gaithersburg, MD). The database includes the gene expression profiles, generated by
5 using the Affymetrix Human Genome U95 array, derived from normal and cancer tissue samples from many different organs. Among the tissue samples in the database, applicants analyzed the expression profiles of normal and cancer tissue sets from breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and stomach.

10 The Affymetrix Human Genome U95 array contains 63,175 probe sets. A probe set is a set of probes to detect one transcript (a gene or a cDNA clone), and usually consists of 16-20 oligonucleotide probe pairs. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of average difference. Average difference serves as a relative indicator of the level of expression of a
15 transcript and is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, an absolute call for each gene is made; "Absent"
20 (= not detected), "Present" (= detected) or "Marginal" (= not clearly Absent or Present).

Differential expression of genes between cancerous and normal tissue samples was determined with the following statistical methods. (1) For each probe set, average difference values and absolute calls were determined by Affymetrix Microarray Suite (v4.0). (2) In a given sample set, outliers among the tissue samples were detected by
25 Principal Component Analysis (PCA) using MatLab program (The MathWorks, Inc., Natick, MA). The data points used in the PCA were the average differences of randomly selected probe sets (5,000~6,000 probe sets). Outliers were excluded from further analysis.

(3) Variations of gene expression were analyzed by using the Fold Change Analysis tool of GeneExpress program. The fold change (cancerous/normal) was calculated by comparing the mean average difference for each gene in a cancerous sample set against the mean average difference of that gene in the normal tissue sample set. Genes showing at least 3-fold increases or decreases in expression level were obtained. Genes were included in the analysis if they had a p-value of less than or equal to 0.05 as determined by an Analysis of Variance Test (Steel *et al.*, Principles and Procedures of Statistics: A Biometrical Approach, Third Ed., McGraw-Hill, 1997). (4) Genes showing differential expression in at least 5 different cancer types were selected.

Analysis of the chip data showed that the expression of the marker LFG1 was significantly up-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG1 (SEQ ID NO: 1 or 3) can be measured by chip sequence fragment no. 91875_s_at on Affymetrix GeneChips® U95. The 91875_s_at sequence is derived from the EST AI053741. The expression levels of 91875_s_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 1, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold change greater than 1.5 was considered to be significant (Wodicka *et al.* (1997), *Nature Biotech.* 15:1359-1367). Also indicated in the Table 1 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that up-regulation of LFG1 may be diagnostic for cancer.

TABLE 1

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	22.71	34	8	4	22		
	INFILTRATING DUCT CARCINOMA	184.04	61	61	0	0	8.11 ^{up}	0
	INFILTRATING LOBULAR CARCINOMA	104.36	10	9	0	1	4.60 ^{up}	0.00456
COLON	NORMAL TISSUE, NOS	76.46	24	23	0	1		
	ADENOCARCINOMA, NOS	244.76	36	35	0	1	3.20 ^{up}	0.00001
ESOPHAGUS	NORMAL TISSUE, NOS	50.47	18	16	1	1		
	ADENOCARCINOMA, NOS	297.56	8	8	0	0	5.90 ^{up}	0.00367
KIDNEY	NORMAL TISSUE, NOS	20.00	25	1	0	24		
	CLEAR CELL CARCINOMA	60.48	11	10	1	0	3.02 ^{up}	0.00082
	RENAL CELL CARCINOMA	65.01	16	13	0	3	3.25 ^{up}	0.00011
LIVER	NORMAL TISSUE, NOS	22.06	19	3	0	16		
	HEPATOCELLULAR CARCINOMA, NOS	86.74	23	21	0	2	3.93 ^{up}	0
LUNG	NORMAL TISSUE, NOS	21.27	32	6	0	26		
	ADENOCARCINOMA, NOS	122.81	39	38	0	1	5.77 ^{up}	0
OVARY	NORMAL TISSUE, NOS	20.21	23	0	0	23		
	PAPILLARY SEROUS ADENOCARCINOMA	112.80	23	21	0	2	5.58 ^{up}	0
PANCREAS	NORMAL TISSUE, NOS	20.02	20	1	0	19		
	ADENOCARCINOMA, NOS	72.55	25	22	0	3	3.62 ^{up}	0
RECTUM	NORMAL TISSUE, NOS	78.86	20	20	0	0		
	ADENOCARCINOMA, NOS	259.95	22	22	0	0	3.30 ^{up}	0.00008
STOMACH	NORMAL TISSUE, NOS	36.06	18	7	0	11		
	ADENOCARCINOMA, NOS	218.74	38	36	0	2	6.07 ^{up}	0

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 91875_s_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GCTGAAGCAGGAAAATCGCTT-3' (SEQ ID NO: 17) and 5'-TGAGACGGAGTCTCACTCGGT-3' (SEQ ID NO: 18))
 5 designed based on the sequence information file of the specific Affymetrix fragment (91875_s_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides
 10 the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, kidney, liver, lung, ovary, stomach and pancreas (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the up-regulation of LFG1 in
 15 cancer compared to normal samples.

EXAMPLE 2: Cloning of Full-Length Human cDNA (LFG1) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 1 or 3 was obtained by polymerase chain reaction (PCR) and rapid amplification of cDNA ends (RACE) using cDNA library from
 20 human heart (ResGen, Huntsville, AL). Gene-specific oligos for PCR (5'-CACCCCTTGCCTCTGTCACTTCCGCA-3' (SEQ ID NO: 21), 5'-GCTGGAGCACCAGGACTGCATTG-3' (SEQ ID NO: 22), 5'-GGAGCTGAGCAGCAGTGTAATGAA-3' (SEQ ID NO: 23), 5'-GAGGCCTGCCTGAAGGAGGAGCTTC-3' (SEQ ID NO: 24), 5'-
 25 TCTGGAAGTAGTGACAGACGCCTCAGG-3' (SEQ ID NO: 25), 5'-AGCCAACGTCGGCTTTGTTATCCAGC-3' (SEQ ID NO: 26), 5'-

GCTGTCAGATATGATGGTTCTGGAC-3' (SEQ ID NO: 27), 5'-
 CCAGCCTCACCCTGTTGGGTTGC-3' (SEQ ID NO: 28), 5'-
 CATTCTCTGAGCTGTATTAGTGT-3' (SEQ ID NO: 29), 5'-
 CCTGAGCTGGAATGACCTGCA-3' (SEQ ID NO: 30), 5'-
 5 CTTTGTGTTGGCTGCAGCCACA-3' (SEQ ID NO: 31), 5'-
 TGAGGAGAGACTTTGCTGACTGGT-3' (SEQ ID NO: 32), 5'-
 GTCCTGTCTGGCGGTGCCGA-3' (SEQ ID NO: 33), 5'-
 GCTCCAGGATCCCCTGTCACCTGGGCCTTCTGCCTTTTGGCT-3' (SEQ ID NO: 34),
 5'-CCATATGGAGAGGAGAGCAGCGGGCCCA-3' (SEQ ID NO: 35), 5'-
 10 GAAGGAGGAACATGGAGAGGAGA-3' (SEQ ID NO: 36), 5'-
 CCATATGCCCCGGGTAGTCTACTGCAT-3' (SEQ ID NO: 37), and 5'-
 GTCGACTCGAGTCACTTCCGCAAAAACCTTCTTG-3' (SEQ ID NO: 38)) and RACE
 (5'-TCCATTCCGAAGGCTCTCCTCC-3' (SEQ ID NO: 39), 5'-
 GTCTGTGTGACGGAAATGTAAGC-3' (SEQ ID NO: 40), and 5'-
 15 GAAGGTCGAAGGCAGACCGATGT-3' (SEQ ID NO: 41)) were designed based on
 predicted genes containing the 91875_s_at sequence using Human Genome Browser
 (University of California, Santa Cruz). The amplified products with the primers were
 incorporated into PCR4-Topo vector using Topo Cloning System (Invitrogen, Carlsbad,
 CA), and followed by sequencing.

20 The nucleotide sequence of the full-length human cDNAs corresponding to the
 differentially regulated mRNA detected above is set forth in SEQ ID NOS: 1 and 3. In the
 former, the cDNA comprises 5293 base pairs. In the latter, the cDNA comprises 5317 base
 pairs.

25 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 1, at
 nucleotides 390-4880 (390-4883 including the stop codon), encodes a protein of 1497
 amino acids. The amino acid sequence corresponding to a predicted protein encoded by
 SEQ ID NO: 1 is set forth in SEQ ID NO: 2. Figure 2 shows the results of a hydrophobicity

analysis of the amino acid sequence of SEQ ID NO: 2 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

5 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 3, at nucleotides 12-4904 (12-4907 including the stop codon), encodes a protein of 1631 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 3 is set forth in SEQ ID NO: 4. Figure 3 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 4 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce
10 antigenic peptides, as described above.

The protein sequence of SEQ ID NO: 2 is identical to that of SEQ ID NO: 4, except that SEQ ID NO: 2 lacks the first 134 amino acids at the N-terminus of SEQ ID NO: 4.

SEQ ID NOS: 2 and 4 contain Calponin homology domain (amino acid positions 38-145 of SEQ ID NO: 4), IQ domain for calmodulin-binding (amino acid positions 629-646 of
15 SEQ ID NO: 2 and amino acid positions 763-780 of SEQ ID NO: 4), RasGAP domain (amino acid positions 858-1195 of SEQ ID NO: 2 and amino acid positions 992-1329 of SEQ ID NO: 4), and RasGAP C-terminal domain (amino acid positions 1298-1421 of SEQ ID NO: 2 and amino acid positions 1432-1555 of SEQ ID NO: 4). SEQ ID NOS: 2 and 4 are similar to IQGAP proteins (Weissbach *et al.* (1994), *J Biol Chem* 269:20517-20521;
20 Brill *et al.* (1996), *Mol Cell Biol* 16:4869-4878). IQGAP binds to and modulate the function of proteins involved in cytoskeletal structure, cell-cell adhesion, and proliferation signaling (Fukada *et al.* (2002), *Cell* 109: 1-20; Briggs *et al.* (2002), *J Biol Chem* 277: 7453-7465; McCallum *et al.* (1998), *J Biol Chem* 273: 22537-22544). IQGAP1-deficient mice exhibited a significant increase in late-onset gastric hyperplasia relative to wild-type (Li *et al.* (2000), *Mol Cell Biol* 20: 697-701).
25

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG1. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and an EST containing 91875_s _at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed three transcripts for this gene, which are approximately 7.2 kb, and 6.3 kb in size. This corresponds to the sizes of the LFG1 clones (SEQ ID NO: 1 and 3).

10 EXAMPLE 3: Identification of Differentially Expressed mRNA in Cancers - 2

The process in EXAMPLE 1 was repeated except that the marker LFG2 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG2 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG2 (SEQ ID NO: 5) can be measured by chip sequence fragment no. 82941_at on Affymetrix GeneChips® U95. The 82941_at sequence is derived from the EST AI277612. The expression levels of 82941_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 2, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the Table 2 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG2 may be diagnostic for cancer.

TABLE 2

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples				Fold Change	Direction	p-value
			Total	Present	Marginal	Absent			
BREAST	NORMAL TISSUE, NOS	1147.66	34	34	0	0			
	INFILTRATING DUCT CARCINOMA	129.77	61	26	3	32	8.71	down	0
	INFILTRATING LOBULAR CARCINOMA	183.37	10	6	1	3	5.48	down	0.00002
COLON	NORMAL TISSUE, NOS	890.06	24	23	1	0			
	ADENOCARCINOMA, NOS	163.35	36	17	1	18	5.39	down	0
ESOPHAGUS	NORMAL TISSUE, NOS	612.34	18	18	0	0			
	ADENOCARCINOMA, NOS	265.11	8	7	1	0	2.31	down	0.02218
LIVER	NORMAL TISSUE, NOS	182.73	19	11	1	7			
	HEPATOCELLULAR CARCINOMA, NOS	114.69	23	7	1	15	1.51	down	0.01211
LUNG	NORMAL TISSUE, NOS	535.84	32	30	2	0			
	ADENOCARCINOMA, NOS	119.36	39	17	3	19	4.27	down	0
LYMPH NODE	NORMAL TISSUE, NOS	454.08	9	7	0	2			
	MALIGNANT LYMPHOMA, NOS	123.13	12	5	0	7	3.24	down	0.02245
OVARY	NORMAL TISSUE, NOS	279.99	23	21	0	2			
	PAPILLARY SEROUS ADENOCARCINOMA	85.45	23	7	1	15	3.5	down	0
PROSTATE	NORMAL TISSUE, NOS	195.77	19	13	1	5			
	ADENOCARCINOMA, NOS	80.06	19	2	2	15	2.57	down	0.00011
RECTUM	NORMAL TISSUE, NOS	943.86	20	19	0	1			
	ADENOCARCINOMA, NOS	176.45	22	13	2	7	5.2	down	0
STOMACH	NORMAL TISSUE, NOS	414.40	18	16	0	2			
	ADENOCARCINOMA, NOS	125.39	38	17	2	19	3.21	down	0

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 82941_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GAATGTGTCAGAGACAAGTGCAGC-3' (SEQ ID NO: 42) and 5'-TGTAGAAACTCTTGGACTAATGGAGG-3' (SEQ ID NO: 43)) designed based on the sequence information file of the EST containing the Affymetrix fragment (82941_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, liver, lung, ovary, and stomach (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG2 in cancer compared to normal samples.

EXAMPLE 4: Cloning of Full-Length Human cDNA (LFG2) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 5 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GAATGTGTCAGAGACAAGTGCAGC-3' (SEQ ID NO: 42)) was designed based on the sequence of the EST containing 82941_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a poorly differentiated stomach adenocarcinoma library (NCI CGAP Gas4) (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating.

The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

5 The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 5. The cDNA comprises 3608 base pairs.

10 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 5, at nucleotides 424-1908 (424-1911 including the stop codon), encodes a protein of 495 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 5 is set forth in SEQ ID NO: 6.

15 SEQ ID NO: 6 has homology to scavenger receptors, which are involved in endocytosis of selected polyanionic ligands, phagocytosis of apoptotic cells and bacteria, cell adhesion, and development of atherosclerosis (Peiser *et al.* (2002), *Curr. Opin. Immunol.* 14:123-128; Resnick *et al.* (1994), *Trends Biol. Sci.* 19:5-8). Based on published studies of scavenger receptors, SEQ ID NO: 6 contains a cytoplasmic domain (amino acid positions 1-35), a transmembrane domain (amino acid positions 36-58), an α -helical coiled-coil domain (amino acid positions 90-301), a collagen-like domain (amino acid positions 305-380), and a scavenger receptor cystein-rich (SRCR) domain (amino acid positions 393-20 493). The SRCR domain contains six cysteine residues (amino acid positions 418, 431, 462, 472, 482, and 492), which may participate in intradomain disulfide bonds. SEQ ID NO: 6 also exhibits homology to a mouse homologue (GenBank Accession No. BC016096). It shows 70% identity over the entire contiguous sequence.

25 Figure 4 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 6 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.*

157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG2. A Northern blot containing total RNAs from various human tissues was used (Human MTN Blot, Clontech, Palo Alto, CA), and the EST containing 82941_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 3.7 kb in size. This corresponds to the size of the LFG2 clone (SEQ ID NO: 5).

EXAMPLE 5: Identification of Differentially Expressed mRNA in Cancers - 3

The process in EXAMPLE 1 was repeated except that the marker LFG3 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG3 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG3 (SEQ ID NO: 7) can be measured by chip sequence fragment no. 46104_at on Affymetrix GeneChips® U95. The 46104_at sequence is derived from the EST AA772055. The expression levels of 46104_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 3, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the

Table 3 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG3 may be diagnostic for cancer.

TABLE 3

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	64.52	34	31	0	3		
	INFILTRATING DUCT CARCINOMA	27.24	61	18	1	42	2.25 down	0
	INFILTRATING LOBULAR CARCINOMA	29.52	10	4	0	6	2.21 down	0.00004
COLON	NORMAL TISSUE, NOS	315.46	24	24	0	0		
	ADENOCARCINOMA, NOS	102.99	36	31	0	5	3.02 down	0.00016
ESOPHAGUS	NORMAL TISSUE, NOS	272.48	18	17	0	1		
	ADENOCARCINOMA, NOS	41.25	8	6	0	2	6.60 down	0.00001
KIDNEY	NORMAL TISSUE, NOS	2626.88	25	25	0	0		
	CLEAR CELL ADENOCARCINOMA, NOS	344.66	11	11	0	0	7.62 down	0.00003
	RENAL CELL CARCINOMA	355.71	16	14	0	2	7.38 down	0.00005
OVARY	NORMAL TISSUE, NOS	1098.41	23	23	0	0		
	PAPILLARY SEROUS ADENOCARCINOMA	178.15	23	22	0	1	6.17 down	0
	NORMAL TISSUE, NOS	274.49	19	19	0	0		
PROSTATE	ADENOCARCINOMA, NOS	117.26	19	18	0	1	2.34 down	0.00016
	NORMAL TISSUE, NOS	410.22	20	20	0	0		
RECTUM	ADENOCARCINOMA, NOS	72.98	22	16	0	6	5.38 down	0
	NORMAL TISSUE, NOS	71.10	18	10	0	8		
STOMACH	ADENOCARCINOMA, NOS	35.49	38	15	1	22	1.96 down	0.00459

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 46104_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GTATGCATCAGAATTCCCTATAGATCTTT-3' (SEQ ID NO: 44) and 5'-TAGATGTTTGGGCAACAGCCT-3' (SEQ ID NO: 45)) designed based on the sequence information file of the EST containing the Affymetrix fragment (46104_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, kidney, ovary, pancreas, and stomach (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG3 in cancer compared to normal samples.

EXAMPLE 6: Cloning of Full-Length Human cDNA (LFG3) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 7 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GTATGCATCAGAATTCCCTATAGATCTTT-3' (SEQ ID NO: 44)) was designed based on the sequence of the EST containing 46104_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from human fetal kidney (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was

screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing. The 5'-end of LFG3 was identified by rapid amplification of cDNA ends (RACE) using the cDNA prepared from human fetal kidney (Clontech, Palo Alto, CA) and a gene specific primer (5'-
 5 TTCCTTCACCAAAGGCATCCAGCCATTCTATG-3' (SEQ ID NO: 46)).

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 7. The cDNA comprises 3162 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 7, at
 10 nucleotides 405-1835 (405-1838 including the stop codon), encodes a protein of 477 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 7 is set forth in SEQ ID NO: 8.

SEQ ID NO: 8 is similar to monocarboxylate transporters (MCTs) and contains ten
 15 predicted transmembrane domains (amino acids positions 10-29, 80-99, 107-128, 140-160, 274-295, 312-332, 339-360, 363-384, 396-416, and 433-451). MCT proteins catalyze the facilitated transport of monocarboxylates such as lactate, pyruvate, branched-chain oxo acids, ketone bodies, beta-hydroxy-butylate, and acetate (Halestrap and Price (1999), *Biochem. J.* 343:281-299). Table 4 summarizes the similarity ratios of SEQ ID NO: 4 with the eight known monocarboxylate transporters.

20

TABLE 4. Homology of LFG3 with MCT proteins

Protein	Size (amino acids)	Identity (%)	Positives (%)
MCT1	500	17.5	34.3
MCT2	478	19.5	35.5
MCT3	504	19.5	34.1
MCT4	465	19.0	33.2

MCT5	487	22.1	36.9
MCT6	505	16.4	31.5
MCT7	523	20.1	35.2
MCT8	613	15.9	27.9

Figure 5 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 8 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG3. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and the EST containing 46104_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 4.2 kb in size. This corresponds to the size of the LFG3 clone (SEQ ID NO: 7).

15 EXAMPLE 7: Identification of Differentially Expressed mRNA in Cancers - 4

The process in EXAMPLE 1 was repeated except that the marker LFG4 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG4 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG4 (SEQ ID NO: 9) can be measured by chip sequence fragment no. 62158_at on Affymetrix GeneChips® U95. The 622158_at sequence is derived from the EST AI123532. The expression levels of 62158_at in various malignant

neoplasms, compared to normal control tissues, are shown in Table 5, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the Table 5 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG4 may be diagnostic for cancer.

TABLE 5

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	156.75	34	33	0	1		
	INFILTRATING DUCT CARCINOMA	90.09	61	51	0	10	1.74 down	0.00001
COLON	NORMAL TISSUE, NOS	234.06	24	22	2	0		
	ADENOCARCINOMA, NOS	64.02	36	24	0	12	3.66 down	0
KIDNEY	NORMAL TISSUE, NOS	134.17	25	23	0	2		
	CLEAR CELL ADENOCARCINOMA, NOS	78.59	11	7	1	3	1.71 down	0.08272
LUNG	RENAL CELL CARCINOMA	55.31	16	9	0	7	2.43 down	0.0021
	NORMAL TISSUE, NOS	179.71	32	32	0	0		
LYMPH NODE	ADENOCARCINOMA, NOS	47.39	39	17	3	19	3.79 down	0
	NORMAL TISSUE, NOS	140.51	9	7	1	1		
OVARY	MALIGNANT LYMPHOMA, NOS	41.43	12	5	1	6	3.39 down	0.00207
	NORMAL TISSUE, NOS	125.19	23	21	0	2		
PROSTATE	PAPILLARY SEROUS ADENOCARCINOMA	37.23	23	4	0	19	3.36 down	0
	NORMAL TISSUE, NOS	191.94	19	18	0	1		
RECTUM	ADENOCARCINOMA, NOS	103.47	19	16	0	3	1.86 down	0.00185
	NORMAL TISSUE, NOS	317.95	20	20	0	0		
STOMACH	ADENOCARCINOMA, NOS	74.28	22	16	1	5	4.28 down	0
	NORMAL TISSUE, NOS	161.77	18	17	0	1		
	ADENOCARCINOMA, NOS	84.55	38	27	2	9	1.91 down	0.0062

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 62158_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-AAATGTCTGATTACCCCATTTTATCAGT-3' (SEQ ID NO: 47) and 5'-
5 TAATCCTGAAATGAACAGCTAACA-3') (SEQ ID NO: 48) designed based on the sequence information file of the EST containing the Affymetrix fragment (62158_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-
10 GTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, liver, lung, ovary, pancreas, and stomach (Ambion,
15 Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG4 in cancer compared to normal samples.

EXAMPLE 8: Cloning of Full-Length Human cDNA (LFG4) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 9 was obtained by rapid amplification of
20 cDNA ends (RACE). Briefly, gene-specific oligos (5'-TAATGTTAGAGTAACAGCATTTTCCTTCAA-3' (SEQ ID NO: 49) and 5'-TGCCCCACACTAACTCAGTTCTTGTGATG-3' (SEQ ID NO: 50)) were designed based on the sequence of the EST containing 62158_at sequence. The oligos was used for PCR amplification of the cDNAs prepared from human brain (Clontech, Palo Alto, CA). The
25 amplified products with the primers were incorporated into PCR4-Topo vector using Topo Cloning System (Invitrogen, Carlsbad, CA), and followed by sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 9. The cDNA comprises 4891 base pairs.

5 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 9, at nucleotides 89-1150 (89-1153 including the stop codon), encodes a protein of 354 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 9 is set forth in SEQ ID NO: 10.

10 SEQ ID NO: 10 is similar to rat Kilon and chicken Neurotractin (Funatsu *et al.* (1999), *J Biol Chem* 274:8224-8230; Marg *et al.* (1999), *J Cell Biol* 145:865-876). Protein sequence analysis reveals a secretory signal peptide (amino acid positions 1-33), three immunoglobulin domains (amino acid positions 47-136, 145-208, and 231-312), and six putative *N*-linked glycosylation sites (amino acid positions 73, 155, 275, 286, 294, and 307). Kilon/Neurotractin is a member of IgLON subfamily of the immunoglobulin superfamily. IgLONs are a family of glycosylphosphatidylinositol (GPI)-linked cell adhesion molecules
15 which are thought to modify neurite outgrowth and might play a role in cell-cell adhesion and recognition (Miyate *et al.* (2000), *J Comparative Neurol* 424:74-85).

Figure 6 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 10 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described
20 above. This hydropathy plot shows the presence of hydrophobic region at the C-terminus. In case of GPI-anchored proteins, the addition of the GPI anchor is known to occur after the cleavage of the C-terminal hydrophobic region. A putative GPI anchor attachment site was found (Gly at the amino acid position 324).

25 Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG4. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and the

EST containing 62158_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single
5 transcript for this gene, which is approximately 5.4 kb in size. This corresponds to the size of the LFG4 clone (SEQ ID NO: 9).

EXAMPLE 9: Identification of Differentially Expressed mRNA in Cancers - 5

The process in EXAMPLE 1 was repeated except that the marker LFG5 was used instead of the marker LFG1.

10 Analysis of the chip data showed that the expression of the marker LFG5 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG5 (SEQ ID NO: 11) can be measured by chip sequence fragment no. 46659_at on Affymetrix GeneChips® U95. The expression levels of 46659_at
15 in various malignant neoplasms, compared to normal control tissues, are shown in Table 6, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. Also indicated in the Table 6 are, for
20 each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that differential regulation of LFG5 may be diagnostic for cancer.

TABLE 6

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal / Absent			
BREAST	NORMAL TISSUE, NOS	152.75	34	31	0	3		
	INFILTRATING DUCT CARCINOMA	404.58	61	60	0	1	2.65 up	0
	INFILTRATING LOBULAR CARCINOMA	277.71	10	10	0	0	1.82 up	0.07445
ESOPHAGUS	NORMAL TISSUE, NOS	85.47	18	15	0	2		
	ADENOCARCINOMA, NOS	373.97	8	8	0	0	4.38 up	0.0009
KIDNEY	NORMAL TISSUE, NOS	53.58	25	17	0	8		
	CLEAR CELL CARCINOMA	161.36	11	11	0	0	3.01 up	0.00011
	RENAL CELL CARCINOMA	249.37	16	16	0	0	4.65 up	0
LUNG	NORMAL TISSUE, NOS	330.65	32	31	0	1		
	ADENOCARCINOMA, NOS	195.43	39	35	0	4	1.69 down	0.00538
LYMPH NODE	NORMAL TISSUE, NOS	219.77	9	9	0	0		
	MALIGNANT LYMPHOMA, NOS	142.09	12	11	0	1	1.55 down	0.25114
OVARY	NORMAL TISSUE, NOS	90.40	23	19	0	4		
	PAPILLARY SEROUS ADENOCARCINOMA	418.81	23	23	0	0	4.63 up	0
PANCREAS	NORMAL TISSUE, NOS	38.53	20	12	0	8		
	ADENOCARCINOMA, NOS	344.37	25	25	0	0	8.94 up	0
STOMACH	NORMAL TISSUE, NOS	185.50	18	17	0	1		
	ADENOCARCINOMA, NOS	279.62	38	35	0	3	1.51 up	0.12664

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 46659_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-AAGGCTTTATCAGGTCTGCATATAGAATC-3' (SEQ ID NO: 51) and 5'-GCAAAGAACCCTAATGCTATTTATCAGC-3' (SEQ ID NO: 52)) designed based on the sequence information file of the specific Affymetrix fragment (46659_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from kidney, lung, ovary, and pancreas (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the differential regulation of LFG5 in cancer compared to normal samples.

EXAMPLE 10: Cloning of Full-Length Human cDNA (LFG5) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 11 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GAGAAGACCAGGGAAGAAGCAG-3' (SEQ ID NO: 53)) was designed based on the sequence of an EST containing 46659_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a human heart library (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was

screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 11. The cDNA
5 comprises 3098 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 11, at nucleotides 223-1569 (223-1572 including the stop codon), encodes a protein of 449 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 11 is set forth in SEQ ID NO: 12.

10 SEQ ID NO: 12 contains a thymidylate kinase domain (amino acid positions 257-438). Thymidylate kinase is a member of nucleotide monophosphate kinases (NMPKs) which play roles in the nucleotide synthesis for RNA and DNA synthesis and are required for the pharmacological activation of therapeutic nucleoside and nucleotide analogs (Van Rompay *et al.* (2000), *Pharmacology & Therapeutics* 87:189-198). SEQ ID NO: 12 exhibits
15 homology to a mouse thymidylate kinase (GenBank Accession No. NM_020557) which is induced during macrophage activation (Lee and O'Brien (1995), *J Immunol.* 154:6094-6102). It shows 63% identity over the entire contiguous sequence.

Figure 7 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 12 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.*
20 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG5. A Northern blot containing total RNAs from various human tissues was used (Human MTN Blot, Clontech, Palo Alto, CA), and an EST
25 containing 82941_at sequence was radioactively labeled by the random primer method and

used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 3.0 kb in size. This corresponds to the size of the LFG5 clone (SEQ ID NO: 11).

EXAMPLE 11: Identification of Differentially Expressed mRNA in Cancers - 6

The process in EXAMPLE 1 was repeated except that the marker LFG6 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG6 was significantly up-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG6 (SEQ ID NO: 13 or 15) can be measured by chip sequence fragment no. 44103_at on Affymetrix GeneChips® U95. The 44103_at sequence is derived from the EST AA865614. The expression levels of 44103_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 7, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold change greater than 1.5 was considered to be significant (Wodicka *et al.* (1997), *Nature Biotech.* 15:1359-1367). Also indicated in the Table 7 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that up-regulation of LFG6 may be diagnostic for cancer.

TABLE 7

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
KIDNEY	NORMAL TISSUE, NOS	337.71	25	25	0	0		
	CLEAR CELL ADENOCARCINOMA, NOS	556.82	11	11	0	0	1.65 up	0.00314
LIVER	NORMAL TISSUE, NOS	406.93	19	18	0	1		
	HEPATOCELLULAR CARCINOMA, NOS	619.40	23	22	0	1	1.52 up	0.00303
OVARY	NORMAL TISSUE, NOS	380.10	23	23	0	0		
	PAPILLARY SEROUS ADENOCARCINOMA	578.60	23	23	0	0	1.52 up	0.00013
	NORMAL TISSUE, NOS	138.75	20	11	1	8		
PANCREAS	ADENOCARCINOMA, NOS	453.01	25	25	0	0	3.26 up	0.00002

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 44103_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GGACGGGGAAGTTGGACGC-3' (SEQ ID NO: 54) and 5'-AAGTGCAGGGCCTCTGGGTG-3' (SEQ ID NO: 55)) designed
5 based on the sequence information file of the specific Affymetrix fragment (44103_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-
10 terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from liver and ovary (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the up-regulation of LFG6 in cancer compared to normal samples.

15 EXAMPLE 12: Cloning of Full-Length Human cDNA (LFG6) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 13 or 15 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-CGCTGGGTCATCGGACGGT-3' (SEQ ID NO: 56)) was
20 designed based on the sequence of an EST containing 44103_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a fully differentiated human stomach adenocarcinoma library (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was
25 converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and

the longest cDNA was screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NOS: 13 and 15. In the former, the cDNA comprises 1893 base pairs. In the latter, the cDNA comprises 1597 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 13, at nucleotides 418-1392 (418-1395 including the stop codon), encodes a protein of 325 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 13 is set forth in SEQ ID NO: 14. Figure 9 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 14 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 15, at nucleotides 271-1431 (271-1434 including the stop codon), encodes a protein of 387 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 15 is set forth in SEQ ID NO: 16. Figure 10 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 16 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

SEQ ID NOS: 14 and 16 contain ubiquitin homologues (UBQ) domain (amino acid positions 239-300). SEQ ID NOS: 14 and 16 are similar to rat Sharpin protein (Lim *et al.* (2001), *Mol Cell Neurosci* 17:385-397). Sharpin directly interacts with the ankyrin repeats of Shank protein which functions in the organization of cytoskeletal complexes and intracellular signaling at specialized cell junctions (Sheng and Kim (2000), *J Cell Sci* 113:1851-1856).

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG6. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and an EST containing 44103_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed three transcripts for this gene, which are approximately 2.2 kb, 1.5 kb, and 1.2 kb in size. This corresponds to the sizes of the LFG6 clones (SEQ ID NO: 13 and 15).

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule selected from the group consisting of: (a) an isolated nucleic acid molecule comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, (b) an isolated nucleic acid molecule encoding SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, (c) an isolated nucleic acid molecule that encodes a protein that is expressed in cancer and that exhibits at least about 75% nucleotide sequence identity over the entire contiguous sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, and (d) an isolated nucleic acid molecule comprising the complement of a nucleic acid molecule of (a), (b) or (c).
2. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises nucleotides 390-4880 of SEQ ID NO: 1, nucleotides 12-4904 of SEQ ID NO: 3, nucleotides 424-1908 of SEQ ID NO: 5, nucleotides 405-1835 of SEQ ID NO: 7, nucleotides 89-1150 of SEQ ID NO: 9, nucleotides 223-1569 of SEQ ID NO: 11, nucleotides 418-1392 of SEQ ID NO: 13, or nucleotides 271-1431 of SEQ ID NO: 15.
3. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises nucleotides 390-4883 of SEQ ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1911 of SEQ ID NO: 5, nucleotides 405-1838 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1572 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, or nucleotides 271-1434 of SEQ ID NO: 15.
4. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule consists of nucleotides 390-4883 of SEQ ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1908 of SEQ ID NO: 5, nucleotides 405-1835 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1569 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, or nucleotides 271-1434 of SEQ ID NO: 15.
5. The isolated nucleic acid molecule of any one of claims 1-4, wherein said nucleic acid molecule is operably linked to one or more expression control elements.

6. A vector comprising an isolated nucleic acid molecule of any one of claims 1-4.

7. A host cell transformed to contain the nucleic acid molecule of any one of claims 1-4.

5 8. A host cell comprising a vector of claim 6.

9. A host cell of claim 8, wherein said host cell is selected from the group consisting of prokaryotic host cells and eukaryotic host cells.

10 10. A method for producing a polypeptide comprising culturing a host cell transformed with the nucleic acid molecule of any one of claims 1-4 under conditions in which the protein encoded by said nucleic acid molecule is expressed.

11. The method of claim 10, wherein said host cell is selected from the group consisting of prokaryotic host cells and eukaryotic host cells.

12. An isolated polypeptide produced by the method of claim 10.

15 13. An isolated polypeptide or protein selected from the group consisting of a protein comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, and a protein having at least about 75% amino acid sequence identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

14. An isolated antibody or antigen-binding antibody fragment that binds to a polypeptide of claim 13.

20 15. An antibody of claim 14 wherein said antibody is a monoclonal or a polyclonal antibody.

16. A method of identifying an agent which modulates the expression of a nucleic acid encoding a protein of claim 13, comprising:

exposing cells which express the nucleic acid to the agent; and

determining whether the agent modulates expression of said nucleic acid, thereby identifying an agent which modulates the expression of a nucleic acid encoding the protein.

- 5 17. A method of identifying an agent which modulates the level of or at least one activity of a protein of claim 13, comprising:

exposing cells which express the protein to the agent;

- 10 determining whether the agent modulates the level of or at least one activity of said protein, thereby identifying an agent which modulates the level of or at least one activity of the protein.

18. The method of claim 17, wherein the agent modulates one activity of the protein.

19. A method of modulating the expression of a nucleic acid encoding a protein of claim 13, comprising:

- 15 administering an effective amount of an agent which modulates the expression of a nucleic acid encoding the protein.

20. A method of modulating at least one activity of a protein of claim 13, comprising:

- 20 administering an effective amount of an agent which modulates at least one activity of the protein.

21. A method of identifying binding partners for a protein of claim 13, comprising:

exposing said protein to a potential binding partner; and

determining if the potential binding partner binds to said protein, thereby identifying binding partners for the protein.

22. A method of identifying an agent which modulates the interaction between a binding partner of claim 21 and a protein of claim 13, comprising:

5 exposing said protein with said partner to the agent; and

determining whether the agent modulates association of the binding partner with said protein, thereby identifying an agent which modulates association of a binding partner with said protein.

10 23. A method of modulating the interaction between a binding partner of claim 21 and a protein of claim 13, comprising:

administering an effective amount of an agent which modulates association of a binding partner with said protein.

24. A non-human transgenic animal modified to contain a nucleic acid molecule of any of claims 1-4.

15 25. The transgenic animal of claim 24, wherein the nucleic acid molecule contains a mutation that prevents expression of the encoded protein.

26. A method of treating a disease state in a subject, comprising:

20 inserting into a diseased cell a gene construct comprising an isolated nucleic acid molecule of any one of claims 1-4 linked to a promoter or enhancer element such that expression of said nucleic molecule causes suppression of said disease.

27. The method of claim 26, wherein said inserting into a diseased cell is accomplished *in vivo*.

28. The method of claim 26, wherein said inserting into a diseased cell further comprises use of a viral or plasmid agent and is accomplished either *in vitro* or *in vivo*.

29. A method of diagnosing a disease state in a subject, comprising:

determining the level of expression of a nucleic acid molecule or protein of any one of claims 1-4 or 13.

30. The method of claims 26 and 29, wherein the disease state is cancer.

31. The method of claims 26 and 29, wherein the disease state is a malignant neoplasm.

32. The method of claim 31, wherein the malignant neoplasm occurs in the breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach.

33. A composition comprising a diluent and a polypeptide or protein selected from the group consisting of: an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising a fragment of at least 10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; and an isolated polypeptide exhibiting at least about 75% amino acid sequence identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

DRAWINGS

FIG. 1

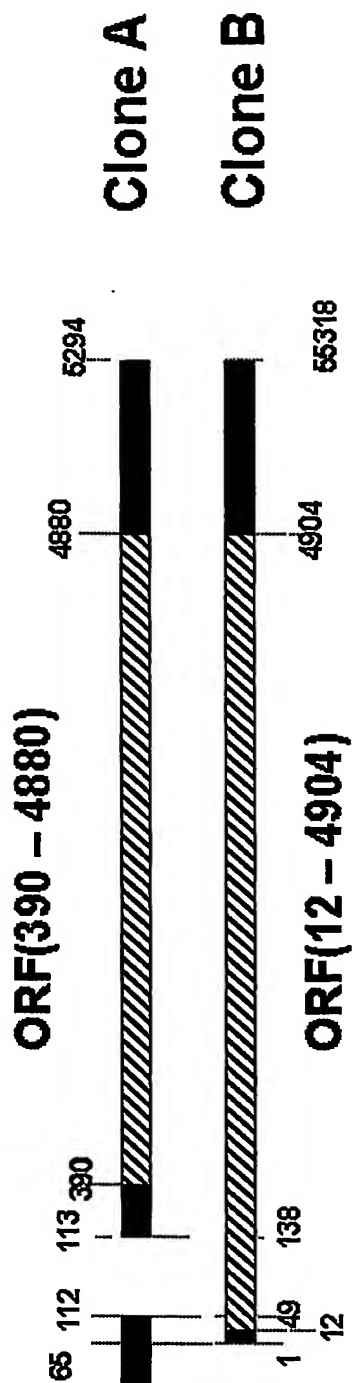


FIG. 2

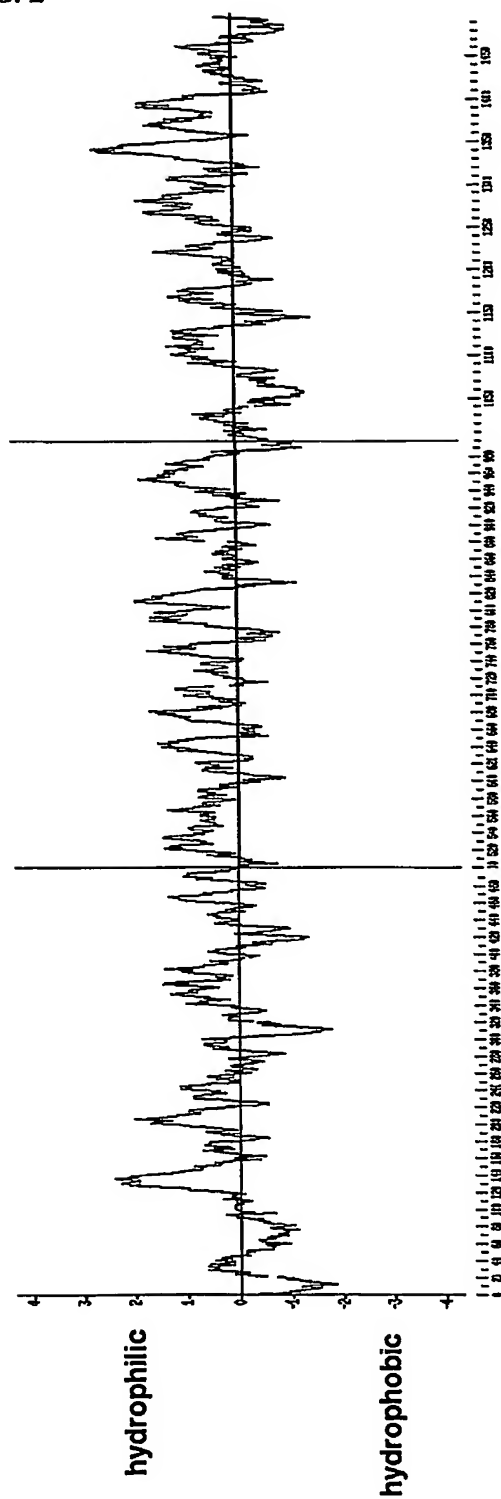


FIG. 3

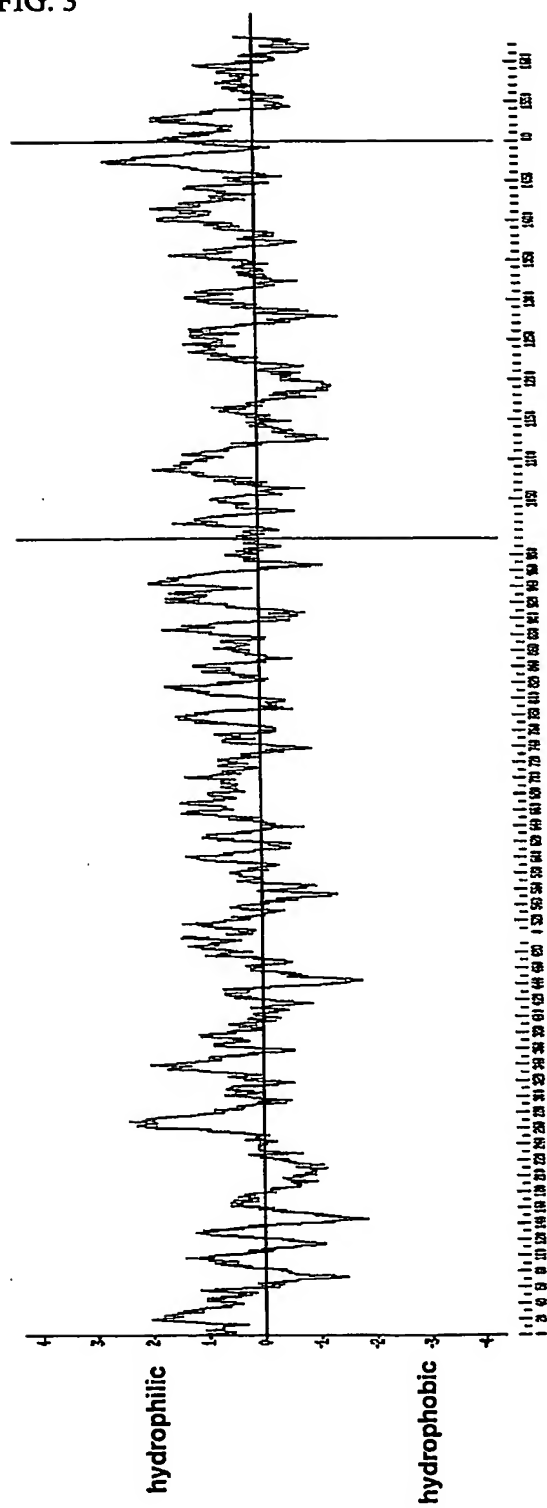


FIG. 4

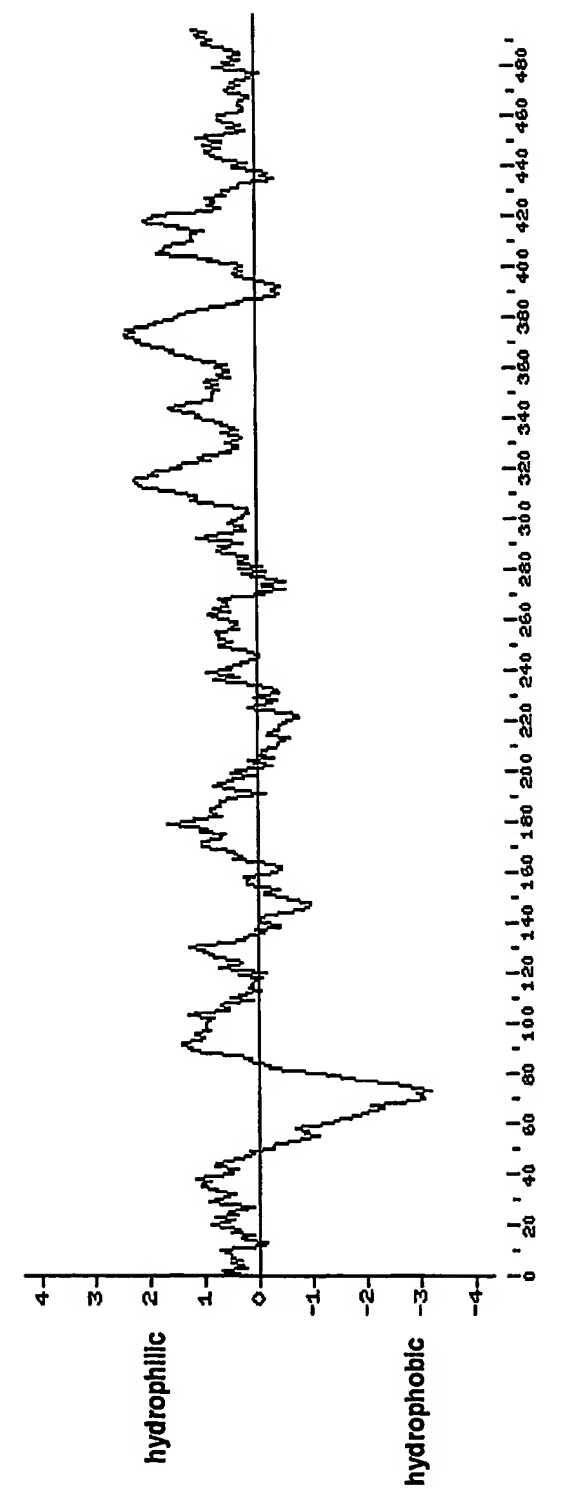


FIG. 5

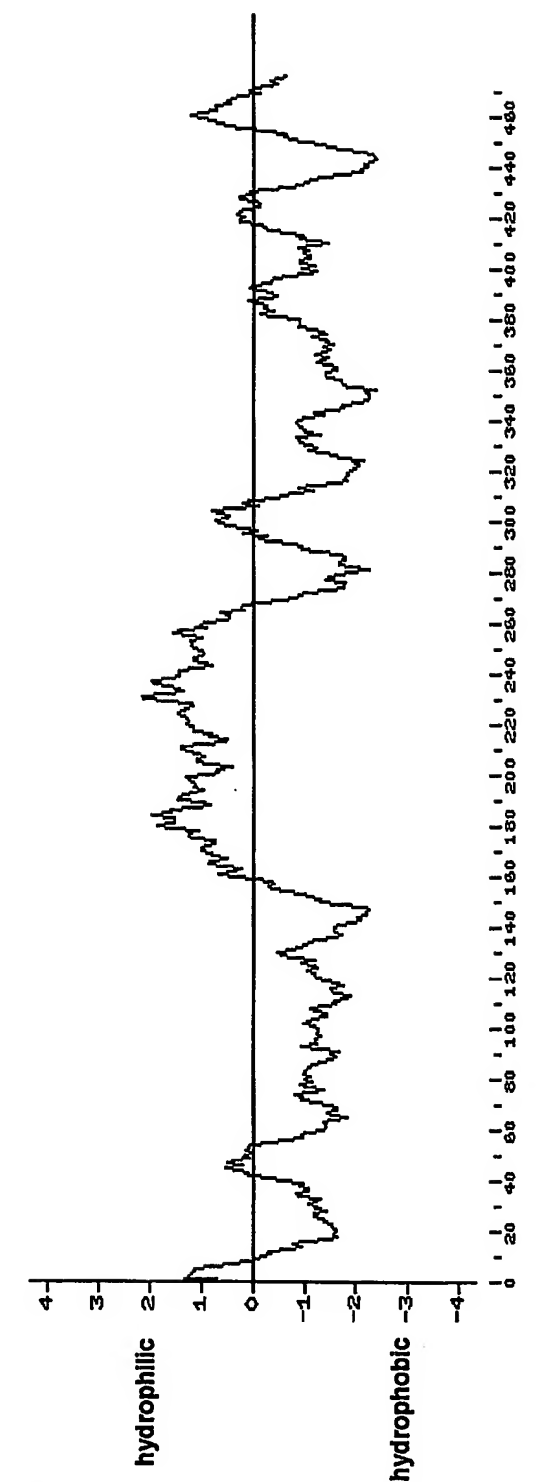


FIG. 6

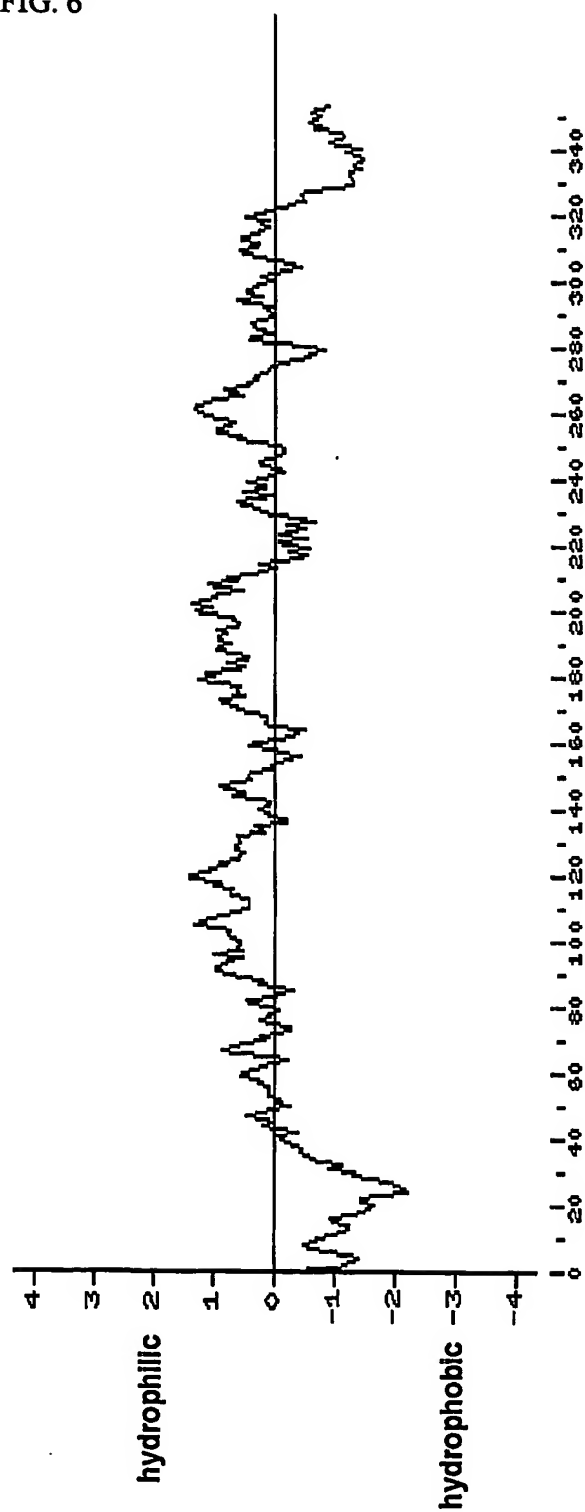


FIG. 7

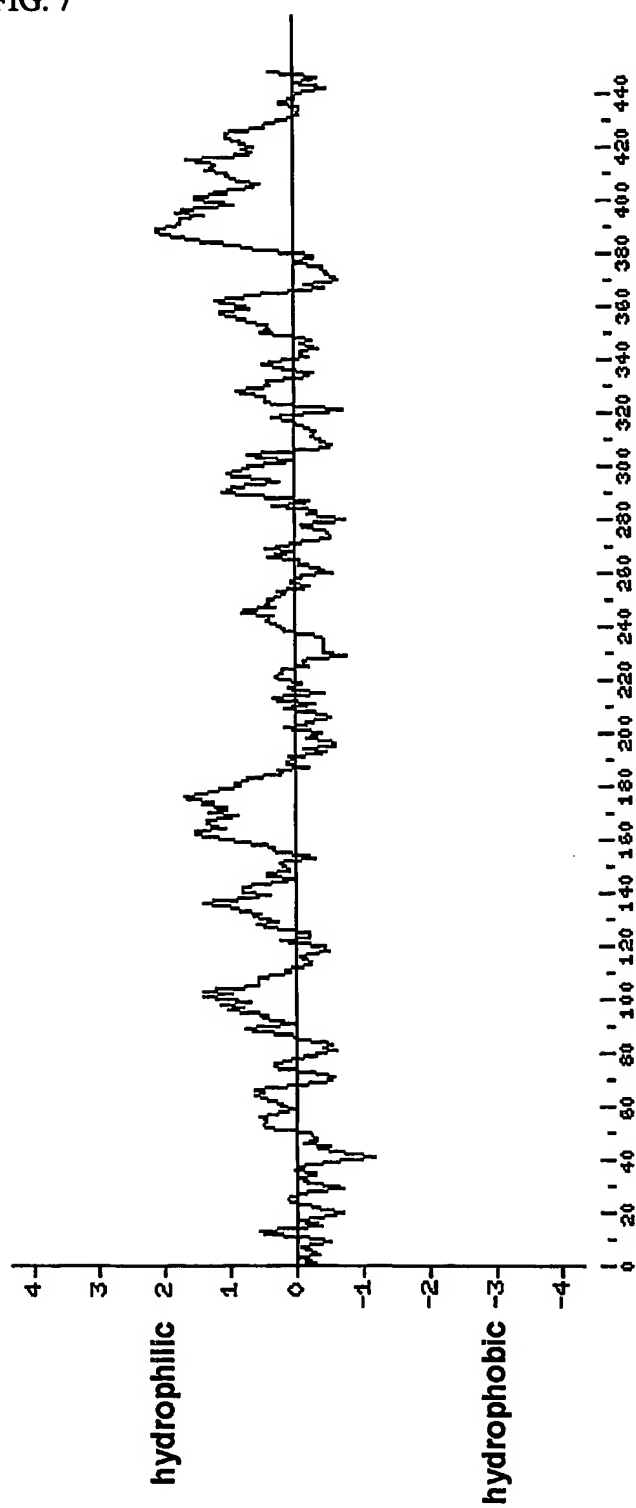


FIG. 8

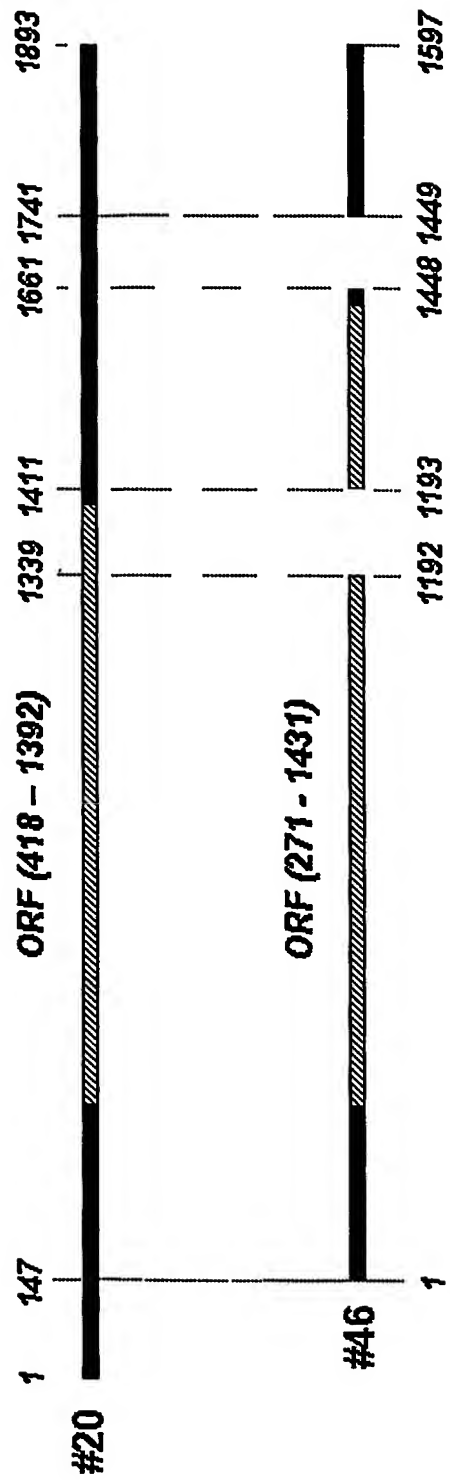


FIG. 9

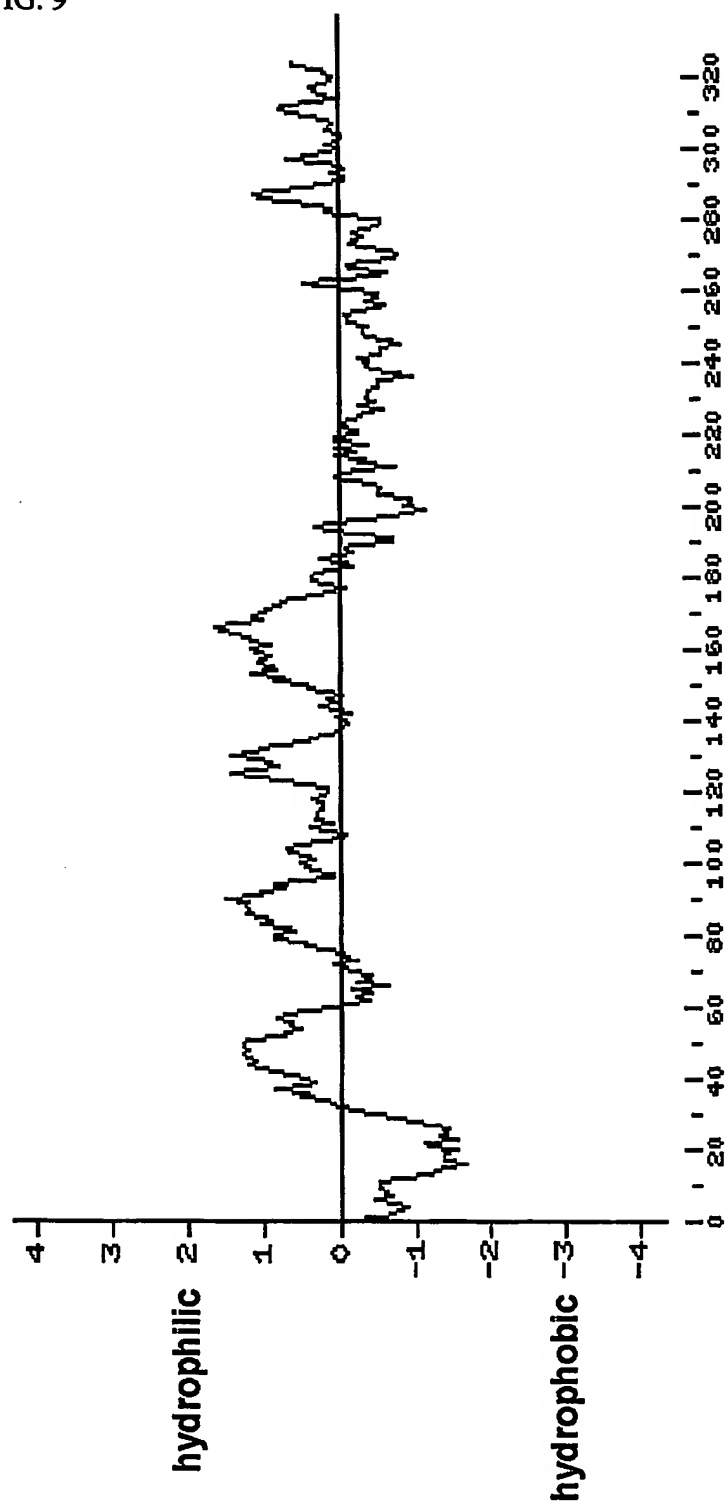
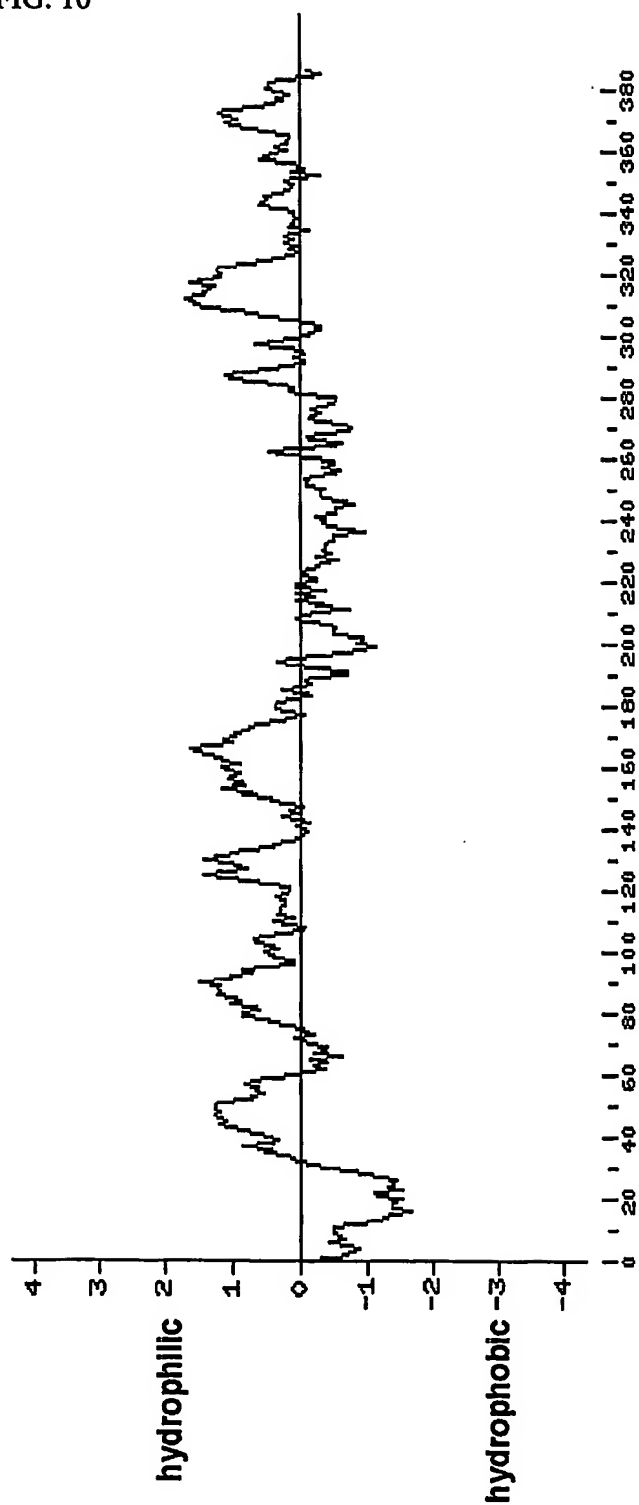


FIG. 10



Sequence Listing

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<120> Gene Families Associated With Cancers

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<150> US60/419912

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<151> 2002-12-16

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<151> 2003-01-03

<160> 56

<170> KopatentIn 1.71

<210> 1

<211> 5293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (390)..(4880)

<223> LBFL109 Clone A

<400> 1

Sequence Listing

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aggcctgcct gaaggaggag ctctcttccc cggtggagct ggaggagagc cttcggaatg	180
gagtgtctgt ggccaagctg ggccactgtt ttgcaccctc cgtgggttccg ttgaagaaga	240
tctacgatgt ggagcagctg cggtaccagg caactggctt acatttccgt cacacagaca	300
acatcaactt ttggctatct gcaatagccc acatcggtct gccttcgacc ttcttcccag	360
agaccacgga catctatgac aaaaagaac atg ccc cgg gta gtc tac tgc atc	413
Met Pro Arg Val Val Tyr Cys Ile	
1 5	
cat gct ctc agt ctc ttc ctc ttc cgg ctg gga ttg gcc cct cag ata	461
His Ala Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala Pro Gln Ile	
10 15 20	
cat gat cta tac ggg aaa gtg aaa ttc aca gct gag gaa ctc agc aac	509
His Asp Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu Leu Ser Asn	
25 30 35 40	
atg gcg tcc gaa ctg gcc aaa tat ggc ctc cag ctg cct gcc ttc agc	557
Met Ala Ser Glu Leu Ala Lys Tyr Gly Leu Gln Leu Pro Ala Phe Ser	
45 50 55	
aag atc ggg ggc atc ttg gcc aat gag ctc tcg gtg gat gag gct gca	605
Lys Ile Gly Gly Ile Leu Ala Asn Glu Leu Ser Val Asp Glu Ala Ala	
60 65 70	
gtc cat gca gct gtt ctt gcc atc aat gaa gca gtg gag cga ggg gtg	653
Val His Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu Arg Gly Val	
75 80 85	
gtg gag gac acc ctg gct gcc ttg cag aat ccc agt gct ctt ctg gag	701
Val Glu Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala Leu Leu Glu	
90 95 100	

Sequence Listing

<p>aat ctc cga gag cct ctg gca gcc gtc tac cag gag atg ctg gcc cag Asn Leu Arg Glu Pro Leu Ala Ala Val Tyr Gln Glu Met Leu Ala Gln 105 110 115 120</p>	749
<p>gcc aag atg gag aag gca gcc aat gcc agg aac cat gat gac aga gaa Ala Lys Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp Asp Arg Glu 125 130 135</p>	797
<p>agc cag gac atc tat gac cac tac cta act cag gct gaa atc cag ggc Ser Gln Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu Ile Gln Gly 140 145 150</p>	845
<p>aat atc aac cat gtc aac gtc cat ggg gct cta gaa gtt gtt gat gat Asn Ile Asn His Val Asn Val His Gly Ala Leu Glu Val Val Asp Asp 155 160 165</p>	893
<p>gcc ctg gaa aga cag agc cct gaa gcc ttg ctc aag gcc ctt caa gac Ala Leu Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala Leu Gln Asp 170 175 180</p>	941
<p>cct gcc ctg gcc ctg cga ggg gtg agg aga gac ttt gct gac tgg tac Pro Ala Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala Asp Trp Tyr 185 190 195 200</p>	989
<p>ctg gag cag ctg aac tca gac aga gag cag aag gca cag gag ctg ggc Leu Glu Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln Glu Leu Gly 205 210 215</p>	1037
<p>ctg gtg gag ctt ctg gaa aag gag gaa gtc cag gct ggt gtg gct gca Leu Val Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly Val Ala Ala 220 225 230</p>	1085
<p>gcc aac aca aag ggt gat cag gaa caa gcc atg ctc cac gct gtg cag Ala Asn Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His Ala Val Gln 235 240 245</p>	1133
<p>cgg atc aac aaa gcc atc cgg agg gga gtg gcg gct gac act gtg aag Arg Ile Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp Thr Val Lys 250 255 260</p>	1181

Sequence Listing

																		1229		
gag ctg atg tgc cct gag gcc cag ctg cct cca gtg tac cct gtt gca																				
Glu Leu Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr Pro Val Ala																				
265	270							275							280					
.																				
tcg tct atg tac cag ctg gag ctg gca gtg ctc cag cag cag cag ggg																			1277	
Ser Ser Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln Gln Gln Gly																				
285							290							295						
gag ctt ggc cag gag gag ctc ttc gtg gct gtg gag atg ctc tca gct																			1325	
Glu Leu Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met Leu Ser Ala																				
300							305							310						
gtg gtc ctg att aac cgg gcc ctg gag gcc cgg gat gcc agt ggc ttc																			1373	
Val Val Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala Ser Gly Phe																				
315							320							325						
tgg agc agc ctg gtg aac cct gcc aca ggc ctg gct gag gtg gaa gga																			1421	
Trp Ser Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu Val Glu Gly																				
330							335							340						
gaa aat gcc cag cgt tac ttc gat gcc ctg ctg aaa ttg cga cag gag																			1469	
Glu Asn Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu Arg Gln Glu																				
345	350							355							360					
cgt ggg atg ggt gag gac ttc ctg agc tgg aat gac ctg cag gcc acc																			1517	
Arg Gly Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu Gln Ala Thr																				
365							370							375						
gtg agc cag gtc aat gca cag acc cag gaa gag act gac cgg gtc ctt																			1565	
Val Ser Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp Arg Val Leu																				
380							385							390						
gca gtc agc ctc atc aat gag gct ctg gac aaa ggc agc cct gag aag																			1613	
Ala Val Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser Pro Glu Lys																				
395							400							405						
act ctg tct gcc cta ctg ctt cct gca gct ggc cta gat gat gtc agc																			1661	
Thr Leu Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp Asp Val Ser																				
410							415							420						

Sequence Listing

ctc cct gtc gcc cct cgg tac cat ctc ctc ctt gtg gca gcc aaa agg	1709
Leu Pro Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala Ala Lys Arg	
425 430 435 440	
cag aag gcc cag gtg aca ggg gat cct gga gct gtg ctg tgg ctt gag	1757
Gln Lys Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu Trp Leu Glu	
445 450 455	
gag atc cgc cag gga gtg gtc aga gcc aac cag gac act aat aca gct	1805
Glu Ile Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr Asn Thr Ala	
460 465 470	
cag aga atg gct ctt ggt gtg gct gcc atc aat caa gcc atc aag gag	1853
Gln Arg Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala Ile Lys Glu	
475 480 485	
ggc aag gca gcc cag act gag cgg gtg ttg agg aac ccc gca gtg gcc	1901
Gly Lys Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro Ala Val Ala	
490 495 500	
ctt cga ggg gta gtt ccc gac tgt gcc aac ggc tac cag cga gcc ctg	1949
Leu Arg Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln Arg Ala Leu	
505 510 515 520	
gaa agt gcc atg gca aag aaa cag cgt cca gca gac aca gct ttc tgg	1997
Glu Ser Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr Ala Phe Trp	
525 530 535	
gtt caa cat gac atg aag gat ggc act gcc tac tac ttc cat ctg cag	2045
Val Gln His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe His Leu Gln	
540 545 550	
acc ttc cag ggg atc tgg gag caa cct cct ggc tgc ccc ctc aac acc	2093
Thr Phe Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro Leu Asn Thr	
555 560 565	
tct cac ctg acc cgg gag gag atc cag tca gct gtc acc aag gtc act	2141
Ser His Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr Lys Val Thr	
570 575 580	

Sequence Listing

gct gcc tat gac cgc caa cag ctc tgg aaa gcc aac gtc ggc ttt gtt	2189
Ala Ala Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val Gly Phe Val	
585 590 595 600	
atc cag ctc cag gcc cgc ctc cgt ggc ttc cta gtt cgg cag aag ttt	2237
Ile Gln Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg Gln Lys Phe	
605 610 615	
gct gag cat tcc cac ttt ctg agg acc tgg ctc cca gca gtc atc aag	2285
Ala Glu His Ser His Phe Leu Arg Thr Trp Leu Pro Ala Val Ile Lys	
620 625 630	
atc cag gct cat tgg cgg ggt tat agg cag cgg aag att tac ctg gag	2333
Ile Gln Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile Tyr Leu Glu	
635 640 645	
tgg ttg cag tat ttt aaa gca aac ctg gat gcc ata atc aag atc cag	2381
Trp Leu Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile Lys Ile Gln	
650 655 660	
gcc tgg gcc cgg atg tgg gca gct cgg agg caa tac ctg agg cgt ctg	2429
Ala Trp Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu Arg Arg Leu	
665 670 675 680	
cac tac ttc cag aag aat gtt aac tcc att gtg aag atc cag gca ttt	2477
His Tyr Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile Gln Ala Phe	
685 690 695	
ttc cga gcc agg aaa gcc caa gat gac tac agg ata tta gtg cat gca	2525
Phe Arg Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu Val His Ala	
700 705 710	
ccc cac cct cct ctc agt gtg gta cgc aga ttt gcc cat ctc ttg aat	2573
Pro His Pro Pro Leu Ser Val Val Arg Arg Phe Ala His Leu Leu Asn	
715 720 725	
caa agc cag caa gac ttc ttg gct gag gca gag ctg ctg aag ctc cag	2621
Gln Ser Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu Lys Leu Gln	
730 735 740	

Sequence Listing

gaa gag gta gtt agg aag atc cga tcc aat cag cag ctg gag cag gac	2669
Glu Glu Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu Glu Gln Asp	
745 750 755 760	
ctc aac atc atg gac atc aag att ggc ctg ctg gtg aag aac cgg atc	2717
Leu Asn Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Arg Ile	
765 770 775	
act ctg cag gaa gtg gtc tcc cac tgc aag aag ctg acc aag agg aat	2765
Thr Leu Gln Glu Val Val Ser His Cys Lys Lys Leu Thr Lys Arg Asn	
780 785 790	
aag gaa cag ctg tca gat atg atg gtt ctg gac aag cag aag ggt tta	2813
Lys Glu Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln Lys Gly Leu	
795 800 805	
aag tcg ctg agc aaa gag aaa cgg cag aaa cta gaa gca tac caa cac	2861
Lys Ser Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala Tyr Gln His	
810 815 820	
ctc ttc tac ctg ctc cag act cag ccc atc tac ctg gcc aag ctg atc	2909
Leu Phe Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala Lys Leu Ile	
825 830 835 840	
ttt cag atg cca cag aac aaa acc acc aag ttc atg gag gca gtg att	2957
Phe Gln Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu Ala Val Ile	
845 850 855	
ttc agc ctg tac aac tat gcc tcc agc cgc cga gag gcc tat ctc ctg	3005
Phe Ser Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala Tyr Leu Leu	
860 865 870	
ctc cag ctg ttc aag aca gca ctc cag gag gaa atc aag tca aag gtg	3053
Leu Gln Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val	
875 880 885	
gag cag ccc cag gac gtg gtg aca ggc aac cca aca gtg gtg agg ctg	3101
Glu Gln Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val Val Arg Leu	
890 895 900	

Sequence Listing

gtg gtg aga ttc tac cgt aat ggg cgg gga cag agt gcc ctg cag gag Val Val Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala Leu Gln Glu 905 910 915 920	3149
att ctg ggc aag gtt atc cag gat gtg cta gaa gac aaa gtg ctc agc Ile Leu Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys Val Leu Ser 925 930 935	3197
gtc cac aca gac cct gtc cac ctc tat aag aac tgg atc aac cag act Val His Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile Asn Gln Thr 940 945 950	3245
gag gcc cag aca ggg cag cgc agc cat ctc cca tat gat gtc acc ccg Glu Ala Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp Val Thr Pro 955 960 965	3293
gag cag gcc ttg agc cac ccc gag gtc cag aga cga ctg gac atc gcc Glu Gln Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu Asp Ile Ala 970 975 980	3341
cta cgc aac ctc ctc gcc atg act gat aag ttc ctt tta gcc atc acc Leu Arg Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu Ala Ile Thr 985 990 995 1000	3389
tca tct gtg gac caa att ccg tat ggg atg cga tat gtg gcc aaa gtc Ser Ser Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val Ala Lys Val 1005 1010 1015	3437
ctg aag gca act ctg gca gag aaa ttc cct gac gcc aca gac agc gag Leu Lys Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr Asp Ser Glu 1020 1025 1030	3485
gtc tat aag gtg gtc ggg aac ctc ctg tac tac cgc ttc ctg aac cca Val Tyr Lys Val Val Gly Asn Leu Leu Tyr Tyr Arg Phe Leu Asn Pro 1035 1040 1045	3533
gct gtg gtg gct cct gac gcc ttc gac att gtg gcc atg gca gct ggt Ala Val Val Ala Pro Asp Ala Phe Asp Ile Val Ala Met Ala Ala Gly 1050 1055 1060	3581

Sequence Listing

gga gcc ctg gct gcc ccc cag cgc cat gcc ctg ggg gct gtg gct cag Gly Ala Leu Ala Ala Pro Gln Arg His Ala Leu Gly Ala Val Ala Gln 1065 1070 1075 1080	3629
ctc cta cag cac gct gcg gct ggc aag gcc ttc tct ggg cag agc cag Leu Leu Gln His Ala Ala Ala Gly Lys Ala Phe Ser Gly Gln Ser Gln 1085 1090 1095	3677
cac cta cgg gtc ctg aat gac tat ctg gag gaa aca cac ctc aag ttc His Leu Arg Val Leu Asn Asp Tyr Leu Glu Glu Thr His Leu Lys Phe 1100 1105 1110	3725
agg aag ttc atc cat aga gcc tgc cag gtg cca gag cca gag gag cgt Arg Lys Phe Ile His Arg Ala Cys Gln Val Pro Glu Pro Glu Glu Arg 1115 1120 1125	3773
ttt gca gtg gac gag tac tca gac atg gtg gct gtg gcc aaa ccc atg Phe Ala Val Asp Glu Tyr Ser Asp Met Val Ala Val Ala Lys Pro Met 1130 1135 1140	3821
gtg tac atc acc gtg ggg gag ctg gtc aac acg cac agg ctg ttg ctg Val Tyr Ile Thr Val Gly Glu Leu Val Asn Thr His Arg Leu Leu Leu 1145 1150 1155 1160	3869
gag cac cag gac tgc att gcc cct gat cac caa gac ccc ctg cat gag Glu His Gln Asp Cys Ile Ala Pro Asp His Gln Asp Pro Leu His Glu 1165 1170 1175	3917
ctc ctg gag gat ctt ggg gag ctg ccc acc atc cct gac ctt att ggt Leu Leu Glu Asp Leu Gly Glu Leu Pro Thr Ile Pro Asp Leu Ile Gly 1180 1185 1190	3965
gag agc atc gct gca gat ggg cac aca gac ctg agc aag cta gaa gtg Glu Ser Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys Leu Glu Val 1195 1200 1205	4013
tcc ctg acg ctg acc aac aag ttt gaa gga cta gag gca gat gct gat Ser Leu Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala Asp Ala Asp 1210 1215 1220	4061

Sequence Listing

gac tcc aac acc cgt agc ctg ctt ctg agc acc aag cag ctg ttg gcc	4109
Asp Ser Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln Leu Leu Ala	
1225 1230 1235 1240	
gat atc ata cag ttc cat cct ggg gac acc ctc aag gag atc ctg tcc	4157
Asp Ile Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu Ile Leu Ser	
1245 1250 1255	
ctc tcg gct tcc aga gag caa gaa gca gcc cac aag cag ctg atg agc	4205
Ileu Ser Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln Leu Met Ser	
1260 1265 1270	
cga cgc cag gcc tgt aca gcc cag aca ccg gag cca ctg cga cga cac	4253
Arg Arg Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu Arg Arg His	
1275 1280 1285	
cgc tca ctg aca gct cac tcc ctc ctg cca ctg gca gag aag cag cgg	4301
Arg Ser Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu Lys Gln Arg	
1290 1295 1300	
cgc gtc ctg cgg aac ctg cgc cga ctt gaa gcc ctg ggg ttg gtc agc	4349
Arg Val Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly Leu Val Ser	
1305 1310 1315 1320	
gcc aga aat ggc tac cag ggg cta gtg gac gag ctg gcc aag gac atc	4397
Ala Arg Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala Lys Asp Ile	
1325 1330 1335	
cgc aac cag cac aga cac agg cac agg cgg aag gca gag ctg gtg aag	4445
Arg Asn Gln His Arg His Arg His Arg Arg Lys Ala Glu Leu Val Lys	
1340 1345 1350	
ctg cag gcc aca tta cag ggc ctg agc act aag acc acc ttc tat gag	4493
Leu Gln Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr Phe Tyr Glu	
1355 1360 1365	
gag cag ggt gac tac tac agc cag tac atc cgg gcc tgc ctg gac cac	4541
Glu Gln Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys Leu Asp His	
1370 1375 1380	

Sequence Listing

ctg gcc ccc gac tcc aag agt tct ggg aag ggg aag aag cag cct tct Leu Ala Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys Gln Pro Ser 1385 1390 1395 1400	4589
ctt cat tac act gct gct cag ctc ctg gaa aag ggt gtc ttg gtg gaa Leu His Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val Leu Val Glu 1405 1410 1415	4637
att gaa gat ctt ccc gcc tct cac ttc aga aac gtc atc ttt gac atc Ile Glu Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile Phe Asp Ile 1420 1425 1430	4685
acg ccg gga gat gag gca gga aag ttt gaa gta aat gcc aag ttc ctg Thr Pro Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala Lys Phe Leu 1435 1440 1445	4733
ggc gtg gac atg gag cga ttt cag ctt cac tat cag gat ctc ctg cag Gly Val Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp Leu Leu Gln 1450 1455 1460	4781
ctc cag tat gag ggt gtg gct gtc atg aaa ctc ttc aac aag gcc aaa Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn Lys Ala Lys 1465 1470 1475 1480	4829
gtc aat gtc aac ctt ctc atc ttc ctc ctc aac aag aag ttt ttg cgg Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys Phe Leu Arg 1485 1490 1495	4877
aag tgacagaggc aaaggggtgct acccaagccc ctcttacctc tctggatgct Lys	4930
ttctttaaca ctaactcacc actgtgcttc cctgcagaca cccagagctc aggactgggc	4990
aaggcccagg gattctcacc ccttccccag ctgggaggag cttgcctgcc tggccacaga	5050
cagtgtatct tctaattggc taaagtgggc cttgcccaga gtccagctgt gtggctttta	5110
tcatgcatga caaaccctg gctttcctgc cagatggatt ctcacccctt acagctgact	5170
cttcaggca atttccatag atctgcagtc ctgcctctgc cacagtctct ctgttgtccc	5230

Sequence Listing

cacatctacc caacttcctg tactgttgcc cttctgatgt taataaaagc agctgttact 5290

ccc 5293

<210> 2

<211> 1497

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Arg Val Val Tyr Cys Ile His Ala Leu Ser Leu Phe Leu Phe

1 5 10 15

Arg Leu Gly Leu Ala Pro Gln Ile His Asp Leu Tyr Gly Lys Val Lys

20 25 30

Phe Thr Ala Glu Glu Leu Ser Asn Met Ala Ser Glu Leu Ala Lys Tyr

35 40 45

Gly Leu Gln Leu Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn

50 55 60

Glu Leu Ser Val Asp Glu Ala Ala Val His Ala Ala Val Leu Ala Ile

65 70 75 80

Asn Glu Ala Val Glu Arg Gly Val Val Glu Asp Thr Leu Ala Ala Leu

85 90 95

Gln Asn Pro Ser Ala Leu Leu Glu Asn Leu Arg Glu Pro Leu Ala Ala

100 105 110

Val Tyr Gln Glu Met Leu Ala Gln Ala Lys Met Glu Lys Ala Ala Asn

115 120 125

Ala Arg Asn His Asp Asp Arg Glu Ser Gln Asp Ile Tyr Asp His Tyr

130 135 140

Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn His Val Asn Val His

Sequence Listing

145	150	155	160
Gly Ala Leu Glu Val Val Asp Asp Ala Leu Glu Arg Gln Ser Pro Glu			
165	170	175	
Ala Leu Leu Lys Ala Leu Gln Asp Pro Ala Leu Ala Leu Arg Gly Val			
180	185	190	
Arg Arg Asp Phe Ala Asp Trp Tyr Leu Glu Gln Leu Asn Ser Asp Arg			
195	200	205	
Glu Gln Lys Ala Gln Glu Leu Gly Leu Val Glu Leu Leu Glu Lys Glu			
210	215	220	
Glu Val Gln Ala Gly Val Ala Ala Ala Asn Thr Lys Gly Asp Gln Glu			
225	230	235	240
Gln Ala Met Leu His Ala Val Gln Arg Ile Asn Lys Ala Ile Arg Arg			
245	250	255	
Gly Val Ala Ala Asp Thr Val Lys Glu Leu Met Cys Pro Glu Ala Gln			
260	265	270	
Leu Pro Pro Val Tyr Pro Val Ala Ser Ser Met Tyr Gln Leu Glu Leu			
275	280	285	
Ala Val Leu Gln Gln Gln Gln Gly Glu Leu Gly Gln Glu Glu Leu Phe			
290	295	300	
Val Ala Val Glu Met Leu Ser Ala Val Val Leu Ile Asn Arg Ala Leu			
305	310	315	320
Glu Ala Arg Asp Ala Ser Gly Phe Trp Ser Ser Leu Val Asn Pro Ala			
325	330	335	
Thr Gly Leu Ala Glu Val Glu Gly Glu Asn Ala Gln Arg Tyr Phe Asp			
340	345	350	
Ala Leu Leu Lys Leu Arg Gln Glu Arg Gly Met Gly Glu Asp Phe Leu			
355	360	365	

Sequence Listing

Ser Trp Asn Asp Leu Gln Ala Thr Val Ser Gln Val Asn Ala Gln Thr
370 375 380

Gln Glu Glu Thr Asp Arg Val Leu Ala Val Ser Leu Ile Asn Glu Ala
385 390 395 400

Leu Asp Lys Gly Ser Pro Glu Lys Thr Leu Ser Ala Leu Leu Leu Pro
405 410 415

Ala Ala Gly Leu Asp Asp Val Ser Leu Pro Val Ala Pro Arg Tyr His
420 425 430

Leu Leu Leu Val Ala Ala Lys Arg Gln Lys Ala Gln Val Thr Gly Asp
435 440 445

Pro Gly Ala Val Leu Trp Leu Glu Glu Ile Arg Gln Gly Val Val Arg
450 455 460

Ala Asn Gln Asp Thr Asn Thr Ala Gln Arg Met Ala Leu Gly Val Ala
465 470 475 480

Ala Ile Asn Gln Ala Ile Lys Glu Gly Lys Ala Ala Gln Thr Glu Arg
485 490 495

Val Leu Arg Asn Pro Ala Val Ala Leu Arg Gly Val Val Pro Asp Cys
500 505 510

Ala Asn Gly Tyr Gln Arg Ala Leu Glu Ser Ala Met Ala Lys Lys Gln
515 520 525

Arg Pro Ala Asp Thr Ala Phe Trp Val Gln His Asp Met Lys Asp Gly
530 535 540

Thr Ala Tyr Tyr Phe His Leu Gln Thr Phe Gln Gly Ile Trp Glu Gln
545 550 555 560

Pro Pro Gly Cys Pro Leu Asn Thr Ser His Leu Thr Arg Glu Glu Ile
565 570 575

Sequence Listing

Gln Ser Ala Val Thr Lys Val Thr Ala Ala Tyr Asp Arg Gln Gln Leu
 580 585 590

Trp Lys Ala Asn Val Gly Phe Val Ile Gln Leu Gln Ala Arg Leu Arg
 595 600 605

Gly Phe Leu Val Arg Gln Lys Phe Ala Glu His Ser His Phe Leu Arg
 610 615 620

Thr Trp Leu Pro Ala Val Ile Lys Ile Gln Ala His Trp Arg Gly Tyr
 625 630 635 640

Arg Gln Arg Lys Ile Tyr Leu Glu Trp Leu Gln Tyr Phe Lys Ala Asn
 645 650 655

Leu Asp Ala Ile Ile Lys Ile Gln Ala Trp Ala Arg Met Trp Ala Ala
 660 665 670

Arg Arg Gln Tyr Leu Arg Arg Leu His Tyr Phe Gln Lys Asn Val Asn
 675 680 685

Ser Ile Val Lys Ile Gln Ala Phe Phe Arg Ala Arg Lys Ala Gln Asp
 690 695 700

Asp Tyr Arg Ile Leu Val His Ala Pro His Pro Pro Leu Ser Val Val
 705 710 715 720

Arg Arg Phe Ala His Leu Leu Asn Gln Ser Gln Gln Asp Phe Leu Ala
 725 730 735

Glu Ala Glu Leu Leu Lys Leu Gln Glu Glu Val Val Arg Lys Ile Arg
 740 745 750

Ser Asn Gln Gln Leu Glu Gln Asp Leu Asn Ile Met Asp Ile Lys Ile
 755 760 765

Gly Leu Leu Val Lys Asn Arg Ile Thr Leu Gln Glu Val Val Ser His
 770 775 780

Cys Lys Lys Leu Thr Lys Arg Asn Lys Glu Gln Leu Ser Asp Met Met

Sequence Listing

785	790	795	800
Val Leu Asp Lys Gln Lys Gly Leu Lys Ser Leu Ser Lys Glu Lys Arg			
	805	810	815
Gln Lys Leu Glu Ala Tyr Gln His Leu Phe Tyr Leu Leu Gln Thr Gln			
	820	825	830
Pro Ile Tyr Leu Ala Lys Leu Ile Phe Gln Met Pro Gln Asn Lys Thr			
	835	840	845
Thr Lys Phe Met Glu Ala Val Ile Phe Ser Leu Tyr Asn Tyr Ala Ser			
	850	855	860
Ser Arg Arg Glu Ala Tyr Leu Leu Leu Gln Leu Phe Lys Thr Ala Leu			
	865	870	875
			880
Gln Glu Glu Ile Lys Ser Lys Val Glu Gln Pro Gln Asp Val Val Thr			
	885	890	895
Gly Asn Pro Thr Val Val Arg Leu Val Val Arg Phe Tyr Arg Asn Gly			
	900	905	910
Arg Gly Gln Ser Ala Leu Gln Glu Ile Leu Gly Lys Val Ile Gln Asp			
	915	920	925
Val Leu Glu Asp Lys Val Leu Ser Val His Thr Asp Pro Val His Leu			
	930	935	940
Tyr Lys Asn Trp Ile Asn Gln Thr Glu Ala Gln Thr Gly Gln Arg Ser			
	945	950	955
			960
His Leu Pro Tyr Asp Val Thr Pro Glu Gln Ala Leu Ser His Pro Glu			
	965	970	975
Val Gln Arg Arg Leu Asp Ile Ala Leu Arg Asn Leu Leu Ala Met Thr			
	980	985	990
Asp Lys Phe Leu Leu Ala Ile Thr Ser Ser Val Asp Gln Ile Pro Tyr			
	995	1000	1005

Sequence Listing

Gly Met Arg Tyr Val Ala Lys Val Leu Lys Ala Thr Leu Ala Glu Lys
1010 1015 1020

Phe Pro Asp Ala Thr Asp Ser Glu Val Tyr Lys Val Val Gly Asn Leu
1025 1030 1035 1040

Leu Tyr Tyr Arg Phe Leu Asn Pro Ala Val Val Ala Pro Asp Ala Phe
1045 1050 1055

Asp Ile Val Ala Met Ala Ala Gly Gly Ala Leu Ala Ala Pro Gln Arg
1060 1065 1070

His Ala Leu Gly Ala Val Ala Gln Leu Leu Gln His Ala Ala Ala Gly
1075 1080 1085

Lys Ala Phe Ser Gly Gln Ser Gln His Leu Arg Val Leu Asn Asp Tyr
1090 1095 1100

Leu Glu Glu Thr His Leu Lys Phe Arg Lys Phe Ile His Arg Ala Cys
1105 1110 1115 1120

Gln Val Pro Glu Pro Glu Glu Arg Phe Ala Val Asp Glu Tyr Ser Asp
1125 1130 1135

Met Val Ala Val Ala Lys Pro Met Val Tyr Ile Thr Val Gly Glu Leu
1140 1145 1150

Val Asn Thr His Arg Leu Leu Leu Glu His Gln Asp Cys Ile Ala Pro
1155 1160 1165

Asp His Gln Asp Pro Leu His Glu Leu Leu Glu Asp Leu Gly Glu Leu
1170 1175 1180

Pro Thr Ile Pro Asp Leu Ile Gly Glu Ser Ile Ala Ala Asp Gly His
1185 1190 1195 1200

Thr Asp Leu Ser Lys Leu Glu Val Ser Leu Thr Leu Thr Asn Lys Phe
1205 1210 1215

Sequence Listing

Glu Gly Leu Glu Ala Asp Ala Asp Asp Ser Asn Thr Arg Ser Leu Leu
1220 1225 1230

Leu Ser Thr Lys Gln Leu Leu Ala Asp Ile Ile Gln Phe His Pro Gly
1235 1240 1245

Asp Thr Leu Lys Glu Ile Leu Ser Leu Ser Ala Ser Arg Glu Gln Glu
1250 1255 1260

Ala Ala His Lys Gln Leu Met Ser Arg Arg Gln Ala Cys Thr Ala Gln
1265 1270 1275 1280

Thr Pro Glu Pro Leu Arg Arg His Arg Ser Leu Thr Ala His Ser Leu
1285 1290 1295

Leu Pro Leu Ala Glu Lys Gln Arg Arg Val Leu Arg Asn Leu Arg Arg
1300 1305 1310

Leu Glu Ala Leu Gly Leu Val Ser Ala Arg Asn Gly Tyr Gln Gly Leu
1315 1320 1325

Val Asp Glu Leu Ala Lys Asp Ile Arg Asn Gln His Arg His Arg His
1330 1335 1340

Arg Arg Lys Ala Glu Leu Val Lys Leu Gln Ala Thr Leu Gln Gly Leu
1345 1350 1355 1360

Ser Thr Lys Thr Thr Phe Tyr Glu Glu Gln Gly Asp Tyr Tyr Ser Gln
1365 1370 1375

Tyr Ile Arg Ala Cys Leu Asp His Leu Ala Pro Asp Ser Lys Ser Ser
1380 1385 1390

Gly Lys Gly Lys Lys Gln Pro Ser Leu His Tyr Thr Ala Ala Gln Leu
1395 1400 1405

Leu Glu Lys Gly Val Leu Val Glu Ile Glu Asp Leu Pro Ala Ser His
1410 1415 1420

Phe Arg Asn Val Ile Phe Asp Ile Thr Pro Gly Asp Glu Ala Gly Lys

Sequence Listing

1425 1430 1435 1440
 Phe Glu Val Asn Ala Lys Phe Leu Gly Val Asp Met Glu Arg Phe Gln
 1445 1450 1455
 Leu His Tyr Gln Asp Leu Leu Gln Leu Gln Tyr Glu Gly Val Ala Val
 1460 1465 1470
 Met Lys Leu Phe Asn Lys Ala Lys Val Asn Val Asn Leu Leu Ile Phe
 1475 1480 1485
 Leu Leu Asn Lys Lys Phe Leu Arg Lys
 1490 1495

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<220>
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 Met Glu Arg Arg Ala Ala Gly Pro Gly Trp Ala
 1 5 10

 gcc tat gaa cgc ctc aca gct gag gag atg gat gag cag agg cgg cag 92
 Ala Tyr Glu Arg Leu Thr Ala Glu Glu Met Asp Glu Gln Arg Arg Gln
 15 20 25

 aat gtt gcc tat cag tac ctg tgc cgg ctg gag gag gcc aag cgc tgg 140
 Asn Val Ala Tyr Gln Tyr Leu Cys Arg Leu Glu Glu Ala Lys Arg Trp
 30 35 40

 atg gag gcc tgc ctg aag gag gag ctt cct tcc ccg gtg gag ctg gag 188

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Sequence Listing

Glu Ala Ala Val His Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu	
205	210 215
cga ggg gtg gtg gag gac acc ctg gct gcc ttg cag aat ccc agt gct	716
Arg Gly Val Val Glu Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala	
220	225 230 235
ctt ctg gag aat ctc cga gag cct ctg gca gcc gtc tac cag gag atg	764
Leu Leu Glu Asn Leu Arg Glu Pro Leu Ala Ala Val Tyr Gln Glu Met	
	240 245 250
ctg gcc cag gcc aag atg gag aag gca gcc aat gcc agg aac cat gat	812
Leu Ala Gln Ala Lys Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp	
	255 260 265
gac aga gaa agc cag gac atc tat gac cac tac cta act cag gct gaa	860
Asp Arg Glu Ser Gln Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu	
	270 275 280
atc cag ggc aat atc aac cat gtc aac gtc cat ggg gct cta gaa gtt	908
Ile Gln Gly Asn Ile Asn His Val Asn Val His Gly Ala Leu Glu Val	
	285 290 295
gtt gat gat gcc ctg gaa aga cag agc cct gaa gcc ttg ctc aag gcc	956
Val Asp Asp Ala Leu Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala	
300	305 310 315
ctt caa gac cct gcc ctg gcc ctg cga ggg gtg agg aga gac ttt gct	1004
Leu Gln Asp Pro Ala Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala	
	320 325 330
gac tgg tac ctg gag cag ctg aac tca gac aga gag cag aag gca cag	1052
Asp Trp Tyr Leu Glu Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln	
	335 340 345
gag ctg ggc ctg gtg gag ctt ctg gaa aag gag gaa gtc cag gct ggt	1100
Glu Leu Gly Leu Val Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly	
	350 355 360
gtg gct gca gcc aac aca aag ggt gat cag gaa caa gcc atg ctc cac	1148

Sequence Listing

Val Ala Ala Ala Asn Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His	
365	370 375
gct gtg cag cgg atc aac aaa gcc atc cgg agg gga gtg gcg gct gac	1196
Ala Val Gln Arg Ile Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp	
380	385 390 395
act gtg aag gag ctg atg tgc cct gag gcc cag ctg cct cca gtg tac	1244
Thr Val Lys Glu Leu Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr	
	400 405 410
cct gtt gca tcg tct atg tac cag ctg gag ctg gca gtg ctc cag cag	1292
Pro Val Ala Ser Ser Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln	
	415 420 425
cag cag ggg gag ctt ggc cag gag gag ctc ttc gtg gct gtg gag atg	1340
Gln Gln Gly Glu Leu Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met	
	430 435 440
ctc tca gct gtg gtc ctg att aac cgg gcc ctg gag gcc cgg gat gcc	1388
Leu Ser Ala Val Val Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala	
	445 450 455
agt ggc ttc tgg agc agc ctg gtg aac cct gcc aca ggc ctg gct gag	1436
Ser Gly Phe Trp Ser Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu	
460	465 470 475
gtg gaa gga gaa aat gcc cag cgt tac ttc gat gcc ctg ctg aaa ttg	1484
Val Glu Gly Glu Asn Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu	
	480 485 490
cga cag gag cgt ggg atg ggt gag gac ttc ctg agc tgg aat gac ctg	1532
Arg Gln Glu Arg Gly Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu	
	495 500 505
cag gcc acc gtg agc cag gtc aat gca cag acc cag gaa gag act gac	1580
Gln Ala Thr Val Ser Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp	
	510 515 520
cgg gtc ctt gca gtc agc ctc atc aat gag gct ctg gac aaa ggc agc	1628

Sequence Listing

Arg Val Leu Ala Val Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser	
525	530 535
cct gag aag act ctg tct gcc cta ctg ctt cct gca gct ggc cta gat	1676
Pro Glu Lys Thr Leu Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp	
540	545 550 555
gat gtc agc ctc cct gtc gcc cct cgg tac cat ctc ctc ctt gtg gca	1724
Asp Val Ser Leu Pro Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala	
	560 565 570
gcc aaa agg cag aag gcc cag gtg aca ggg gat cct gga gct gtg ctg	1772
Ala Lys Arg Gln Lys Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu	
	575 580 585
tgg ctt gag gag atc cgc cag gga gtg gtc aga gcc aac cag gac act	1820
Trp Leu Glu Glu Ile Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr	
	590 595 600
aat aca gct cag aga atg gct ctt ggt gtg gct gcc atc aat caa gcc	1868
Asn Thr Ala Gln Arg Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala	
	605 610 615
atc aag gag ggc aag gca gcc cag act gag cgg gtg ttg agg aac ccc	1916
Ile Lys Glu Gly Lys Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro	
	620 625 630 635
gca gtg gcc ctt cga ggg gta gtt ccc gac tgt gcc aac ggc tac cag	1964
Ala Val Ala Leu Arg Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln	
	640 645 650
cga gcc ctg gaa agt gcc atg gca aag aaa cag cgt cca gca gac aca	2012
Arg Ala Leu Glu Ser Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr	
	655 660 665
gct ttc tgg gtt caa cat gac atg aag gat ggc act gcc tac tac ttc	2060
Ala Phe Trp Val Gln His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe	
	670 675 680
cat ctg cag acc ttc cag ggg atc tgg gag caa cct cct ggc tgc ccc	2108

Sequence Listing

His Leu Gln Thr Phe Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro	
685	690 695
ctc aac acc tct cac ctg acc cgg gag gag atc cag tca gct gtc acc	2156
Leu Asn Thr Ser His Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr	
700	705 710 715
aag gtc act gct gcc tat gac cgc caa cag ctc tgg aaa gcc aac gtc	2204
Lys Val Thr Ala Ala Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val	
	720 725 730
ggc ttt gtt atc cag ctc cag gcc cgc ctc cgt ggc ttc cta gtt cgg	2252
Gly Phe Val Ile Gln Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg	
	735 740 745
cag aag ttt gct gag cat tcc cac ttt ctg agg acc tgg ctc cca gca	2300
Gln Lys Phe Ala Glu His Ser His Phe Leu Arg Thr Trp Leu Pro Ala	
	750 755 760
gtc atc aag atc cag gct cat tgg cgg ggt tat agg cag cgg aag att	2348
Val Ile Lys Ile Gln Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile	
	765 770 775
tac ctg gag tgg ttg cag tat ttt aaa gca aac ctg gat gcc ata atc	2396
Tyr Leu Glu Trp Leu Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile	
	780 785 790 795
aag atc cag gcc tgg gcc cgg atg tgg gca gct cgg agg caa tac ctg	2444
Lys Ile Gln Ala Trp Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu	
	800 805 810
agg cgt ctg cac tac ttc cag aag aat gtt aac tcc att gtg aag atc	2492
Arg Arg Leu His Tyr Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile	
	815 820 825
cag gca ttt ttc cga gcc agg aaa gcc caa gat gac tac agg ata tta	2540
Gln Ala Phe Phe Arg Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu	
	830 835 840
gtg cat gca ccc cac cct cct ctc agt gtg gta cgc aga ttt gcc cat	2588

Sequence Listing

Val His Ala Pro His Pro Pro Leu Ser Val Val Arg Arg Phe Ala His	
845	850 855
ctc ttg aat caa agc cag caa gac ttc ttg gct gag gca gag ctg ctg	2636
Leu Leu Asn Gln Ser Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu	
860	865 870 875
aag ctc cag gaa gag gta gtt agg aag atc cga tcc aat cag cag ctg	2684
Lys Leu Gln Glu Glu Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu	
	880 885 890
gag cag gac ctc aac atc atg gac atc aag att ggc ctg ctg gtg aag	2732
Glu Gln Asp Leu Asn Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys	
	895 900 905
aac cgg atc act ctg cag gaa gtg gtc tcc cac tgc aag aag ctg acc	2780
Asn Arg Ile Thr Leu Gln Glu Val Val Ser His Cys Lys Lys Leu Thr	
	910 915 920
aag agg aat aag gaa cag ctg tca gat atg atg gtt ctg gac aag cag	2828
Lys Arg Asn Lys Glu Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln	
	925 930 935
aag ggt tta aag tcg ctg agc aaa gag aaa cgg cag aaa cta gaa gca	2876
Lys Gly Leu Lys Ser Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala	
	940 945 950 955
tac caa cac ctc ttc tac ctg ctc cag act cag ccc atc tac ctg gcc	2924
Tyr Gln His Leu Phe Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala	
	960 965 970
aag ctg atc ttt cag atg cca cag aac aaa acc acc aag ttc atg gag	2972
Lys Leu Ile Phe Gln Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu	
	975 980 985
gca gtg att ttc agc ctg tac aac tat gcc tcc agc cgc cga gag gcc	3020
Ala Val Ile Phe Ser Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala	
	990 995 1000
tat ctc ctg ctc cag ctg ttc aag aca gca ctc cag gag gaa atc aag	3068

Sequence Listing

Tyr Leu Leu Leu Gln Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys	
1005	1010 1015
tca aag gtg gag cag ccc cag gac gtg gtg aca ggc aac cca aca gtg	3116
Ser Lys Val Glu Gln Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val	
1020	1025 1030 1035
gtg agg ctg gtg gtg aga ttc tac cgt aat ggg cgg gga cag agt gcc	3164
Val Arg Leu Val Val Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala	
1040	1045 1050
ctg cag gag att ctg ggc aag gtt atc cag gat gtg cta gaa gac aaa	3212
Leu Gln Glu Ile Leu Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys	
1055	1060 1065
gtg ctc agc gtc cac aca gac cct gtc cac ctc tat aag aac tgg atc	3260
Val Leu Ser Val His Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile	
1070	1075 1080
aac cag act gag gcc cag aca ggg cag cgc agc cat ctc cca tat gat	3308
Asn Gln Thr Glu Ala Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp	
1085	1090 1095
gtc acc ccg gag cag gcc ttg agc cac ccc gag gtc cag aga cga ctg	3356
Val Thr Pro Glu Gln Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu	
1100	1105 1110 1115
gac atc gcc cta cgc aac ctc ctc gcc atg act gat aag ttc ctt tta	3404
Asp Ile Ala Leu Arg Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu	
1120	1125 1130
gcc atc acc tca tct gtg gac caa att ccg tat ggg atg cga tat gtg	3452
Ala Ile Thr Ser Ser Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val	
1135	1140 1145
gcc aaa gtc ctg aag gca act ctg gca gag aaa ttc cct gac gcc aca	3500
Ala Lys Val Leu Lys Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr	
1150	1155 1160
gac agc gag gtc tat aag gtg gtc ggg aac ctc ctg tac tac cgc ttc	3548

Sequence Listing

Asp	Ser	Glu	Val	Tyr	Lys	Val	Val	Gly	Asn	Leu	Leu	Tyr	Tyr	Arg	Phe		
1165						1170				1175							
ctg	aac	cca	gct	gtg	gtg	gct	cct	gac	gcc	ttc	gac	att	gtg	gcc	atg		3596
Leu	Asn	Pro	Ala	Val	Val	Ala	Pro	Asp	Ala	Phe	Asp	Ile	Val	Ala	Met		
1180					1185					1190					1195		
gca	gct	ggg	gga	gcc	ctg	gct	gcc	ccc	cag	cgc	cat	gcc	ctg	ggg	gct		3644
Ala	Ala	Gly	Gly	Ala	Leu	Ala	Ala	Pro	Gln	Arg	His	Ala	Leu	Gly	Ala		
				1200					1205				1210				
gtg	gct	cag	ctc	cta	cag	cac	gct	gcg	gct	ggc	aag	gcc	ttc	tct	ggg		3692
Val	Ala	Gln	Leu	Leu	Gln	His	Ala	Ala	Ala	Gly	Lys	Ala	Phe	Ser	Gly		
			1215				1220					1225					
cag	agc	cag	cac	cta	cgg	gtc	ctg	aat	gac	tat	ctg	gag	gaa	aca	cac		3740
Gln	Ser	Gln	His	Leu	Arg	Val	Leu	Asn	Asp	Tyr	Leu	Glu	Glu	Thr	His		
	1230					1235					1240						
ctc	aag	ttc	agg	aag	ttc	atc	cat	aga	gcc	tgc	cag	gtg	cca	gag	cca		3788
Leu	Lys	Phe	Arg	Lys	Phe	Ile	His	Arg	Ala	Cys	Gln	Val	Pro	Glu	Pro		
	1245				1250					1255							
gag	gag	cgt	ttt	gca	gtg	gac	gag	tac	tca	gac	atg	gtg	gct	gtg	gcc		3836
Glu	Glu	Arg	Phe	Ala	Val	Asp	Glu	Tyr	Ser	Asp	Met	Val	Ala	Val	Ala		
1260				1265					1270				1275				
aaa	ccc	atg	gtg	tac	atc	acc	gtg	ggg	gag	ctg	gtc	aac	acg	cac	agg		3884
Lys	Pro	Met	Val	Tyr	Ile	Thr	Val	Gly	Glu	Leu	Val	Asn	Thr	His	Arg		
		1280						1285				1290					
ctg	ttg	ctg	gag	cac	cag	gac	tgc	att	gcc	cct	gat	cac	caa	gac	ccc		3932
Leu	Leu	Leu	Glu	His	Gln	Asp	Cys	Ile	Ala	Pro	Asp	His	Gln	Asp	Pro		
		1295				1300					1305						
ctg	cat	gag	ctc	ctg	gag	gat	ctt	ggg	gag	ctg	ccc	acc	atc	cct	gac		3980
Leu	His	Glu	Leu	Leu	Glu	Asp	Leu	Gly	Glu	Leu	Pro	Thr	Ile	Pro	Asp		
	1310					1315				1320							
ctt	att	ggg	gag	agc	atc	gct	gca	gat	ggg	cac	aca	gac	ctg	agc	aaq		4028

Sequence Listing

Leu Ile Gly Glu Ser Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys	
1325	1330 1335
cta gaa gtg tcc ctg acg ctg acc aac aag ttt gaa gga cta gag gca	4076
Leu Glu Val Ser Leu Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala	
1340	1345 1350 1355
gat gct gat gac tcc aac acc cgt agc ctg ctt ctg agc acc aag cag	4124
Asp Ala Asp Asp Ser Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln	
1360	1365 1370
ctg ttg gcc gat atc ata cag ttc cat cct ggg gac acc ctc aag gag	4172
Leu Leu Ala Asp Ile Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu	
1375	1380 1385
atc ctg tcc ctc tcg gct tcc aga gag caa gaa gca gcc cac aag cag	4220
Ile Leu Ser Leu Ser Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln	
1390	1395 1400
ctg atg agc cga cgc cag gcc tgt aca gcc cag aca ccg gag cca ctg	4268
Leu Met Ser Arg Arg Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu	
1405	1410 1415
cga cga cac cgc tca ctg aca gct cac tcc ctc ctg cca ctg gca gag	4316
Arg Arg His Arg Ser Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu	
1420	1425 1430 1435
aag cag cgg cgc gtc ctg cgg aac ctg cgc cga ctt gaa gcc ctg ggg	4364
Lys Gln Arg Arg Val Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly	
1440	1445 1450
ttg gtc agc gcc aga aat ggc tac cag ggg cta gtg gac gag ctg gcc	4412
Leu Val Ser Ala Arg Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala	
1455	1460 1465
aag gac atc cgc aac cag cac aga cac agg cac agg cgg aag gca gag	4460
Lys Asp Ile Arg Asn Gln His Arg His Arg His Arg Arg Lys Ala Glu	
1470	1475 1480
ctg gtg aag ctg cag gcc aca tta cag ggc ctg agc act aag acc acc	4508

Sequence Listing

Leu Val Lys Leu Gln Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr	
1485	1490 1495
ttc tat gag gag cag ggt gac tac tac agc cag tac atc cgg gcc tgc	4556
Phe Tyr Glu Glu Gln Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys	
1500	1505 1510 1515
ctg gac cac ctg gcc ccc gac tcc aag agt tct ggg aag ggg aag aag	4604
Leu Asp His Leu Ala Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys	
	1520 1525 1530
cag cct tct ctt cat tac act gct gct cag ctc ctg gaa aag ggt gtc	4652
Gln Pro Ser Leu His Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val	
	1535 1540 1545
ttg gtg gaa att gaa gat ctt ccc gcc tct cac ttc aga aac gtc atc	4700
Leu Val Glu Ile Glu Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile	
	1550 1555 1560
ttt gac atc acg ccg gga gat gag gca gga aag ttt gaa gta aat gcc	4748
Phe Asp Ile Thr Pro Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala	
	1565 1570 1575
aag ttc ctg ggt gtg gac atg gag cga ttt cag ctt cac tat cag gat	4796
Lys Phe Leu Gly Val Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp	
	1580 1585 1590 1595
ctc ctg cag ctc cag tat gag ggt gtg gct gtc atg aaa ctc ttc aac	4844
Leu Leu Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn	
	1600 1605 1610
aag gcc aaa gtc aat gtc aac ctt ctc atc ttc ctc ctc aac aag aag	4892
Lys Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys	
	1615 1620 1625
ttt ttg cgg aag	
Phe Leu Arg Lys	4940
	1630
tgacag aggcaaaggg tgctacccaa gccctcttta	
cctctctgga tgctttcttt aacactaact caccactgtg cttccctgca gacaccaga	5000

Sequence Listing

gctcaggact gggcaaggcc cagggattct cacccttcc ccagctggga ggagcttgcc 5060

tgcttgcca cagacagtgt atcttctaataa tggctaaagt ggccttgcc cagagtccag 5120

ctgtgtggct tttatcatgc atgacaaacc cctggcttcc ctgccagatg gattctcatc 5180

ccttacagct gactcttcca ggcaatttcc atagatctgc agtcctgcct ctgccacagt 5240

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aagcagctgt tactccc 5317

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<211> 1631

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Arg Arg Ala Ala Gly Pro Gly Trp Ala Ala Tyr Glu Arg Leu
1 5 10 15

Thr Ala Glu Glu Met Asp Glu Gln Arg Arg Gln Asn Val Ala Tyr Gln
20 25 30

Tyr Leu Cys Arg Leu Glu Glu Ala Lys Arg Trp Met Glu Ala Cys Leu
35 40 45

Lys Glu Glu Leu Pro Ser Pro Val Glu Leu Glu Glu Ser Leu Arg Asn
50 55 60

Gly Val Leu Leu Ala Lys Leu Gly His Cys Phe Ala Pro Ser Val Val
65 70 75 80

Pro Leu Lys Lys Ile Tyr Asp Val Glu Gln Leu Arg Tyr Gln Ala Thr
85 90 95

Gly Leu His Phe Arg His Thr Asp Asn Ile Asn Phe Trp Leu Ser Ala
100 105 110

Sequence Listing

Ile Ala His Ile Gly Leu Pro Ser Thr Phe Phe Pro Glu Thr Thr Asp
115 120 125

Ile Tyr Asp Lys Lys Asn Met Pro Arg Val Val Tyr Cys Ile His Ala
130 135 140

Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala Pro Gln Ile His Asp
145 150 155 160

Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu Leu Ser Asn Met Ala
165 170 175

Ser Glu Leu Ala Lys Tyr Gly Leu Gln Leu Pro Ala Phe Ser Lys Ile
180 185 190

Gly Gly Ile Leu Ala Asn Glu Leu Ser Val Asp Glu Ala Ala Val His
195 200 205

Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu Arg Gly Val Val Glu
210 215 220

Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala Leu Leu Glu Asn Leu
225 230 235 240

Arg Glu Pro Leu Ala Ala Val Tyr Gln Glu Met Leu Ala Gln Ala Lys
245 250 255

Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp Asp Arg Glu Ser Gln
260 265 270

Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile
275 280 285

Asn His Val Asn Val His Gly Ala Leu Glu Val Val Asp Asp Ala Leu
290 295 300

Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala Leu Gln Asp Pro Ala
305 310 315 320

Sequence Listing

Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala Asp Trp Tyr Leu Glu
 325 330 335

Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln Glu Leu Gly Leu Val
 340 345 350

Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly Val Ala Ala Ala Asn
 355 360 365

Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His Ala Val Gln Arg Ile
 370 375 380

Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp Thr Val Lys Glu Leu
 385 390 395 400

Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr Pro Val Ala Ser Ser
 405 410 415

Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln Gln Gln Gly Glu Leu
 420 425 430

Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met Leu Ser Ala Val Val
 435 440 445

Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala Ser Gly Phe Trp Ser
 450 455 460

Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu Val Glu Gly Glu Asn
 465 470 475 480

Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu Arg Gln Glu Arg Gly
 485 490 495

Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu Gln Ala Thr Val Ser
 500 505 510

Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp Arg Val Leu Ala Val
 515 520 525

Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser Pro Glu Lys Thr Leu

Sequence Listing

530	535	540
Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp Asp Val Ser Leu Pro		
545	550	555 560
Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala Ala Lys Arg Gln Lys		
565	570	575
Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu Trp Leu Glu Glu Ile		
580	585	590
Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr Asn Thr Ala Gln Arg		
595	600	605
Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala Ile Lys Glu Gly Lys		
610	615	620
Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro Ala Val Ala Leu Arg		
625	630	635 640
Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln Arg Ala Leu Glu Ser		
645	650	655
Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr Ala Phe Trp Val Gln		
660	665	670
His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe His Leu Gln Thr Phe		
675	680	685
Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro Leu Asn Thr Ser His		
690	695	700
Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr Lys Val Thr Ala Ala		
705	710	715 720
Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val Gly Phe Val Ile Gln		
725	730	735
Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg Gln Lys Phe Ala Glu		
740	745	750

Sequence Listing

His Ser His Phe Leu Arg Thr Trp Leu Pro Ala Val Ile Lys Ile Gln
 755 760 765

Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile Tyr Leu Glu Trp Leu
 770 775 780

Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile Lys Ile Gln Ala Trp
 785 790 795 800

Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu Arg Arg Leu His Tyr
 805 810 815

Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile Gln Ala Phe Phe Arg
 820 825 830

Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu Val His Ala Pro His
 835 840 845

Pro Pro Leu Ser Val Val Arg Arg Phe Ala His Leu Leu Asn Gln Ser
 850 855 860

Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu Lys Leu Gln Glu Glu
 865 870 875 880

Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu Glu Gln Asp Leu Asn
 885 890 895

Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Arg Ile Thr Leu
 900 905 910

Gln Glu Val Val Ser His Cys Lys Lys Leu Thr Lys Arg Asn Lys Glu
 915 920 925

Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln Lys Gly Leu Lys Ser
 930 935 940

Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala Tyr Gln His Leu Phe
 945 950 955 960

Sequence Listing

Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala Lys Leu Ile Phe Gln
965 970 975

Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu Ala Val Ile Phe Ser
980 985 990

Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala Tyr Leu Leu Leu Gln
995 1000 1005

Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val Glu Gln
1010 1015 1020

Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val Val Arg Leu Val Val
1025 1030 1035 1040

Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala Leu Gln Glu Ile Leu
1045 1050 1055

Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys Val Leu Ser Val His
1060 1065 1070

Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile Asn Gln Thr Glu Ala
1075 1080 1085

Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp Val Thr Pro Glu Gln
1090 1095 1100

Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu Asp Ile Ala Leu Arg
1105 1110 1115 1120

Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu Ala Ile Thr Ser Ser
1125 1130 1135

Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val Ala Lys Val Leu Lys
1140 1145 1150

Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr Asp Ser Glu Val Tyr
1155 1160 1165

Lys Val Val Gly Asn Leu Leu Tyr Tyr Arg Phe Leu Asn Pro Ala Val

Sequence Listing

1170	1175	1180
Val Ala Pro Asp Ala Phe Asp Ile Val Ala Met Ala Ala Gly Gly Ala		
1185	1190	1195 1200
Leu Ala Ala Pro Gln Arg His Ala Leu Gly Ala Val Ala Gln Leu Leu		
1205	1210	1215
Gln His Ala Ala Ala Gly Lys Ala Phe Ser Gly Gln Ser Gln His Leu		
1220	1225	1230
Arg Val Leu Asn Asp Tyr Leu Glu Glu Thr His Leu Lys Phe Arg Lys		
1235	1240	1245
Phe Ile His Arg Ala Cys Gln Val Pro Glu Pro Glu Glu Arg Phe Ala		
1250	1255	1260
Val Asp Glu Tyr Ser Asp Met Val Ala Val Ala Lys Pro Met Val Tyr		
1265	1270	1275 1280
Ile Thr Val Gly Glu Leu Val Asn Thr His Arg Leu Leu Leu Glu His		
1285	1290	1295
Gln Asp Cys Ile Ala Pro Asp His Gln Asp Pro Leu His Glu Leu Leu		
1300	1305	1310
Glu Asp Leu Gly Glu Leu Pro Thr Ile Pro Asp Leu Ile Gly Glu Ser		
1315	1320	1325
Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys Leu Glu Val Ser Leu		
1330	1335	1340
Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala Asp Ala Asp Asp Ser		
1345	1350	1355 1360
Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln Leu Leu Ala Asp Ile		
1365	1370	1375
Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu Ile Leu Ser Leu Ser		
1380	1385	1390

Sequence Listing

Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln Leu Met Ser Arg Arg
1395 1400 1405

Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu Arg Arg His Arg Ser
1410 1415 1420

Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu Lys Gln Arg Arg Val
1425 1430 1435 1440

Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly Leu Val Ser Ala Arg
1445 1450 1455

Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala Lys Asp Ile Arg Asn
1460 1465 1470

Gln His Arg His Arg His Arg Arg Lys Ala Glu Leu Val Lys Leu Gln
1475 1480 1485

Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr Phe Tyr Glu Glu Gln
1490 1495 1500

Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys Leu Asp His Leu Ala
1505 1510 1515 1520

Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys Gln Pro Ser Leu His
1525 1530 1535

Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val Leu Val Glu Ile Glu
1540 1545 1550

Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile Phe Asp Ile Thr Pro
1555 1560 1565

Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala Lys Phe Leu Gly Val
1570 1575 1580

Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp Leu Leu Gln Leu Gln
1585 1590 1595 1600

Sequence Listing

Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn Lys Ala Lys Val Asn
 1605 1610 1615

Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys Phe Leu Arg Lys
 1620 1625 1630

<210> 5
 <211> 3608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (424)..(1908)
 <223> Clone LBFL110

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 cctcagaaca tctcctgata gctacccagg accaggcacc aaggacaggg agtcccaggg 120
 gcacaccccc cattctgggt ccccaggcc cagaccccca ctctgccaca ggttgcatact 180
 tgacctgggc ctctgcaga agtggccctc gtggctctgc tctgagactc gtccctgggc 240
 gccctgcag cccctttcta tgactccatc tggatttggc tggtgtggg gacgcggtcc 300
 gaggggcggc ctggctctca gcgtgggtggc agccagctct ctggccacca tggcaaatgc 360
 tgagatctga ggggacaagg ctctacagcc tcagccaggg gactcagct gttgcagggt 420
 gtg atg gag aac aaa gct atg tac cta cac acc gtc agc gac tgt 465
 Met Glu Asn Lys Ala Met Tyr Leu His Thr Val Ser Asp Cys
 1 5 10
 gac acc agc tcc atc tgt gag gat tcc ttt gat ggc agg agc ctg tcc 513

Sequence Listing

Asp	Thr	Ser	Ser	Ile	Cys	Glu	Asp	Ser	Phe	Asp	Gly	Arg	Ser	Leu	Ser		
15					20					25					30		
aag	ctg	aac	ctg	tgt	gag	gat	ggg	cca	tgt	cac	aaa	cgg	cgg	gca	agc		561
Lys	Leu	Asn	Leu	Cys	Glu	Asp	Gly	Pro	Cys	His	Lys	Arg	Arg	Ala	Ser		
				35				40						45			
atc	tgc	tgt	acc	cag	ctg	ggg	tcc	ctg	tgc	gcc	ctg	aag	cat	gct	gtc		609
Ile	Cys	Cys	Thr	Gln	Leu	Gly	Ser	Leu	Ser	Ala	Leu	Lys	His	Ala	Val		
			50					55					60				
ctg	ggg	ctc	tac	ctg	ctg	gtc	ttc	ctg	att	ctt	gtg	ggc	atc	ttc	atc		657
Leu	Gly	Leu	Tyr	Leu	Leu	Val	Phe	Leu	Ile	Leu	Val	Gly	Ile	Phe	Ile		
			65				70					75					
tta	gca	gtg	tcc	agg	ccg	cgc	agc	tcc	cct	gac	gac	ctg	aag	gcc	ctg		705
Leu	Ala	Val	Ser	Arg	Pro	Arg	Ser	Ser	Pro	Asp	Asp	Leu	Lys	Ala	Leu		
			80				85					90					
act	cgc	aat	gtg	aac	cgg	ctg	aat	gag	agc	ttc	cgg	gac	ttg	cag	ctg		753
Thr	Arg	Asn	Val	Asn	Arg	Leu	Asn	Glu	Ser	Phe	Arg	Asp	Leu	Gln	Leu		
			95			100				105					110		
cgg	ctg	ctg	cag	gct	ccg	ctg	caa	gcg	gac	ctg	acg	gag	cag	gtg	tgg		801
Arg	Leu	Leu	Gln	Ala	Pro	Leu	Gln	Ala	Asp	Leu	Thr	Glu	Gln	Val	Trp		
				115					120					125			
aag	gtg	cag	gac	gcg	ctg	cag	aac	cag	tca	gac	tgc	ttg	ctg	gcg	ctg		849
Lys	Val	Gln	Asp	Ala	Leu	Gln	Asn	Gln	Ser	Asp	Ser	Leu	Leu	Ala	Leu		
			130					135					140				
gcg	ggc	gca	gtg	cag	cgg	ctg	gag	ggc	gcg	ctg	tgg	ggg	ctg	cag	gcg		897
Ala	Gly	Ala	Val	Gln	Arg	Leu	Glu	Gly	Ala	Leu	Trp	Gly	Leu	Gln	Ala		
			145				150					155					
cag	gcg	gtg	cag	acc	gag	cag	gcg	gtg	gcc	ctg	ctg	cgg	gac	cgc	acg		945
Gln	Ala	Val	Gln	Thr	Glu	Gln	Ala	Val	Ala	Leu	Leu	Arg	Asp	Arg	Thr		
			160				165				170						
ggc	cag	cag	agc	gac	acg	gcg	cag	ctg	gag	ctc	tac	cag	ctg	cag	gtg		993

Sequence Listing

Gly Gln Gln Ser Asp Thr Ala Gln Leu Glu Leu Tyr Gln Leu Gln Val	
175	180 185 190
gag agc aac agt agc cag ctg ctg ctg agg cgc cac gcg ggc ctg ctg	1041
Glu Ser Asn Ser Ser Gln Leu Leu Leu Arg Arg His Ala Gly Leu Leu	
195	200 205
gac ggg ctg gcg cgc agg gtg ggc atc ctg ggc gag gag ctg gcc gac	1089
Asp Gly Leu Ala Arg Arg Val Gly Ile Leu Gly Glu Glu Leu Ala Asp	
210	215 220
gtg ggc ggc gtg ctg cgc ggc ctc aac cac agc ctg tcc tac gac gtg	1137
Val Gly Gly Val Leu Arg Gly Leu Asn His Ser Leu Ser Tyr Asp Val	
225	230 235
gcc ctc cac cgc acg cgg ctg cag gac ctg cgg gtg ctg gtg agc aac	1185
Ala Leu His Arg Thr Arg Leu Gln Asp Leu Arg Val Leu Val Ser Asn	
240	245 250
gcc agc gag gac acg cgc cgc ctg cgc ctg gcg cac gta ggc atg gag	1233
Ala Ser Glu Asp Thr Arg Arg Leu Arg Leu Ala His Val Gly Met Glu	
255	260 265 270
ctg cag ctg aag cag gag ctg gcc atg ctc aac gcg gtc acc gag gac	1281
Leu Gln Leu Lys Gln Glu Leu Ala Met Leu Asn Ala Val Thr Glu Asp	
275	280 285
ctg cgc ctc aag gac tgg gag cac tcc atc gca ctg cgg aac atc tcc	1329
Leu Arg Leu Lys Asp Trp Glu His Ser Ile Ala Leu Arg Asn Ile Ser	
290	295 300
ctc gcg aaa ggg cca ccg gga ccc aaa ggt gat cag ggg cat gaa gga	1377
Leu Ala Lys Gly Pro Pro Gly Pro Lys Gly Asp Gln Gly His Glu Gly	
305	310 315
aag gaa ggc agg cct ggc atc cct gga ttg cct gga ctt cga ggt ctg	1425
Lys Glu Gly Arg Pro Gly Ile Pro Gly Leu Pro Gly Leu Arg Gly Leu	
320	325 330
ccc ggg gag aga ggt acc cca gga ttg ccc ggg ccc aag ggc gat gat	1473

Sequence Listing

Pro Gly Glu Arg Gly Thr	Pro Gly Leu Pro Gly	Pro Lys Gly Asp Asp	
335	340	345	350
ggg aag ctg ggg gcc aca gga cca atg ggc atg cgt ggg ttc aaa ggt			1521
Gly Lys Leu Gly Ala Thr Gly Pro Met Gly Met Arg Gly Phe Lys Gly			
355	360	365	
gac cga ggc cca aaa gga gag aaa gga gag aaa gga gac aga gct ggg			1569
Asp Arg Gly Pro Lys Gly Glu Lys Gly Glu Lys Gly Asp Arg Ala Gly			
370	375	380	
gat gcc agt ggc gtg gag gcc ccg atg atg atc cgc ctg gtg aat ggc			1617
Asp Ala Ser Gly Val Glu Ala Pro Met Met Ile Arg Leu Val Asn Gly			
385	390	395	
tca ggt ccg cac gag ggc cgc gtg gaa gtg tac cac gac cgg cgt tgg			1665
Ser Gly Pro His Glu Gly Arg Val Glu Val Tyr His Asp Arg Arg Trp			
400	405	410	
ggc acc gtg tgt gac gac ggc tgg gac aag aag gac gga gac gtg gtg			1713
Gly Thr Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val			
415	420	425	430
tgc cgc atg ctc ggc ttc cgc ggt gtg gag gag gtg tac cgc aca gct			1761
Cys Arg Met Leu Gly Phe Arg Gly Val Glu Glu Val Tyr Arg Thr Ala			
435	440	445	
cga ttc ggg caa ggc act ggg agg atc tgg atg gat gac gtt gcc tgc			1809
Arg Phe Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Ala Cys			
450	455	460	
aag ggc aca gag gaa acc atc ttc cgc tgc agc ttc tcc aaa tgg ggg			1857
Lys Gly Thr Glu Glu Thr Ile Phe Arg Cys Ser Phe Ser Lys Trp Gly			
465	470	475	
gtg aca aac tgt gga cat gcc gaa gat gcc agc gtg aca tgc aac aga			1905
Val Thr Asn Cys Gly His Ala Glu Asp Ala Ser Val Thr Cys Asn Arg			
480	485	490	
cac	tg aaagtgggca gagcccaagt tcggggctcct gcacagagca cccttcctgc		1960

Sequence Listing

His

495

atccctgggg tggggcacag ctcggggcca ccctgaccat gcctcgacca caccctgtcc	2020
agcattctca gtcctcacac ctgcatccca ggaccgtggg ggccggtcgt catttcctc	2080
ttgaacatgt gctccgaagt ataactctgg gacctactgc ccgtctctct cttccaccag	2140
gttcctgcat gaggagccct gatcaactgg atcaccactt tgcccagcct ctgaacacca	2200
tgcaccaggc ctcaatatcc cagttccctt tggcctttta gttacagggtg aatgctgaga	2260
atgtgtcaga gacaagtgca gcagcagcga tggttggtag tatagatcat ttactcttca	2320
gacaattccc aaacctccat tagtccaaga gtttctacat cttcctcccc agcaagaggc	2380
aacgtcaagt gatgaatttc cccctttac tctgcctctg ctccccattt gctagtttga	2440
ggaagtgaca tagaggagaa gccagctgta ggggcaagag ggaaatgcaa gtcacctgca	2500
ggaatccagc tagatttgga gaagggaatg aaactaacat tgaatgacta ccatggcacg	2560
ctaaatagta tcttgggtgc caaattcatg tatccactta gctgcattgg tccagggcat	2620
gtcagtctgg atacagcctt acctccaggt agcacttaac tgggtccattc acctagactg	2680
caagtaagaa gacaaaatga ctgagaccgt gtgccacct gaacttattg tctttacttg	2740
gcctgagcta aaagcttggg tgcaggacct gtgtaactag aaagttgcct acttcagaac	2800
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ctggcattgg gcagtcacgg ttaaagccaa gtcattgtgt tctcagctgt ttggagggtga	2980
tgattttgca tcttccaagc ctcttcaggt gtgaatctgt ggtcaggaaa acacaagtcc	3040
taatggaacc cttagggggg aaggaaatga agattcccta taacctctgg ggggtggggag	3100

Sequence Listing

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taggaataag gggcttgggc ctccataaat ctgcaatctg caccctcctc ctagagacag      3160
ggagatcgtg ttctgctttt tacatgagga gcagaactgg gccatacaca tgttcaagaa      3220
ctaggggagc tacctggtag caagtgagtg cagacccacc tcacctggg ggaatctcaa      3280
actcataggc ctcagatata cgatcacctg tcatatcagg tgagcactgg cctgcttggg      3340
gagagacctg ggcccctcca ggtgtaggaa cagcaacact cctggctgac aactaagcca      3400
atatggccct aggtcattct tgcttccaat atgcttgcca ctccttaaata gtcctaataga      3460
tgagaaactc tctttctgac caattgctat gtttacataa cagcatgta ctcatgcatc      3520
ccttgccaga gcccatatat gtatgcatat ataaacatag cactttttac tacatagctc      3580
agcacattgc aaggtttgca tttaagtt      3608

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<210> 6
 <211> 495
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Glu Asn Lys Ala Met Tyr Leu His Thr Val Ser Asp Cys Asp Thr
 1 5 10 15
 Ser Ser Ile Cys Glu Asp Ser Phe Asp Gly Arg Ser Leu Ser Lys Leu
 20 25 30
 Asn Leu Cys Glu Asp Gly Pro Cys His Lys Arg Arg Ala Ser Ile Cys
 35 40 45
 Cys Thr Gln Leu Gly Ser Leu Ser Ala Leu Lys His Ala Val Leu Gly
 50 55 60
 Leu Tyr Leu Leu Val Phe Leu Ile Leu Val Gly Ile Phe Ile Leu Ala
 65 70 75 80

Sequence Listing

Val Ser Arg Pro Arg Ser Ser Pro Asp Asp Leu Lys Ala Leu Thr Arg
85 90 95

Asn Val Asn Arg Leu Asn Glu Ser Phe Arg Asp Leu Gln Leu Arg Leu
100 105 110

Leu Gln Ala Pro Leu Gln Ala Asp Leu Thr Glu Gln Val Trp Lys Val
115 120 125

Gln Asp Ala Leu Gln Asn Gln Ser Asp Ser Leu Leu Ala Leu Ala Gly
130 135 140

Ala Val Gln Arg Leu Glu Gly Ala Leu Trp Gly Leu Gln Ala Gln Ala
145 150 155 160

Val Gln Thr Glu Gln Ala Val Ala Leu Leu Arg Asp Arg Thr Gly Gln
165 170 175

Gln Ser Asp Thr Ala Gln Leu Glu Leu Tyr Gln Leu Gln Val Glu Ser
180 185 190

Asn Ser Ser Gln Leu Leu Leu Arg Arg His Ala Gly Leu Leu Asp Gly
195 200 205

Leu Ala Arg Arg Val Gly Ile Leu Gly Glu Glu Leu Ala Asp Val Gly
210 215 220

Gly Val Leu Arg Gly Leu Asn His Ser Leu Ser Tyr Asp Val Ala Leu
225 230 235 240

His Arg Thr Arg Leu Gln Asp Leu Arg Val Leu Val Ser Asn Ala Ser
245 250 255

Glu Asp Thr Arg Arg Leu Arg Leu Ala His Val Gly Met Glu Leu Gln
260 265 270

Leu Lys Gln Glu Leu Ala Met Leu Asn Ala Val Thr Glu Asp Leu Arg
275 280 285

Sequence Listing

Leu Lys Asp Trp Glu His Ser Ile Ala Leu Arg Asn Ile Ser Leu Ala
290 295 300

Lys Gly Pro Pro Gly Pro Lys Gly Asp Gln Gly His Glu Gly Lys Glu
305 310 315 320

Gly Arg Pro Gly Ile Pro Gly Leu Pro Gly Leu Arg Gly Leu Pro Gly
325 330 335

Glu Arg Gly Thr Pro Gly Leu Pro Gly Pro Lys Gly Asp Asp Gly Lys
340 345 350

Leu Gly Ala Thr Gly Pro Met Gly Met Arg Gly Phe Lys Gly Asp Arg
355 360 365

Gly Pro Lys Gly Glu Lys Gly Glu Lys Gly Asp Arg Ala Gly Asp Ala
370 375 380

Ser Gly Val Glu Ala Pro Met Met Ile Arg Leu Val Asn Gly Ser Gly
385 390 395 400

Pro His Glu Gly Arg Val Glu Val Tyr His Asp Arg Arg Trp Gly Thr
405 410 415

Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val Cys Arg
420 425 430

Met Leu Gly Phe Arg Gly Val Glu Glu Val Tyr Arg Thr Ala Arg Phe
435 440 445

Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Ala Cys Lys Gly
450 455 460

Thr Glu Glu Thr Ile Phe Arg Cys Ser Phe Ser Lys Trp Gly Val Thr
465 470 475 480

Asn Cys Gly His Ala Glu Asp Ala Ser Val Thr Cys Asn Arg His
485 490 495

Sequence Listing

<210> 7
 <211> 3162
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (405)..(1835)
 <223> Clone LBFL123

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gcgggaccga ttgcctaata ctccggcagg ggccggggcc gcagctggct cggataaata	240
gccgcccggc tggcccgag ctgcagggga gagcggcggc cgcgatcccc accacaccac	300
cagcccggcc gcacggggca ctgagccggg tgctgagcac cggaggcccc gccgaggccg	360
ggactcagga cctgcagaga aacgcctcct gattttgtct taca atg gaa ctt	413
	Met Glu Leu
	1
aaa aag tcg cct gac ggt gga tgg ggc tgg gtg att gtg ttt gtc tcc	461
Lys Lys Ser Pro Asp Gly Gly Trp Gly Trp Val Ile Val Phe Val Ser	
5 10 15	
ttc ctt act cag ttt ttg tgt tac gga tcc cca cta gct gtt gga gtc	509
Phe Leu Thr Gln Phe Leu Cys Tyr Gly Ser Pro Leu Ala Val Gly Val	
20 25 30 35	
ctg tac ata gaa tgg ctg gat gcc ttt ggt gaa gga aaa gga aaa aca	557
Leu Tyr Ile Glu Trp Leu Asp Ala Phe Gly Glu Gly Lys Gly Lys Thr	
40 45 50	

Sequence Listing

gcc tgg gtt gga tcc ctg gca agt gga gtt ggc ttg ctt gca agt cct Ala Trp Val Gly Ser Leu Ala Ser Gly Val Gly Leu Leu Ala Ser Pro	605
55 60 65	
gtc tgc agt ctc tgt gtc tca tct ttt gga gca aga cct gtc aca atc Val Cys Ser Leu Cys Val Ser Ser Phe Gly Ala Arg Pro Val Thr Ile	653
70 75 80	
ttc agt ggc ttc atg gtg gct gga ggc ctg atg ttg agc agt ttt gct Phe Ser Gly Phe Met Val Ala Gly Gly Leu Met Leu Ser Ser Phe Ala	701
85 90 95	
ccc aat atc tac ttt ctg ttt ttt tcc tat ggc att gtt gta ggt tca Pro Asn Ile Tyr Phe Leu Phe Phe Ser Tyr Gly Ile Val Val Gly Ser	749
100 105 110 115	
agc gtt ggc ctt ttc ata tat gct gct ctg cag agg atg ctg gtt gag Ser Val Gly Leu Phe Ile Tyr Ala Ala Leu Gln Arg Met Leu Val Glu	797
120 125 130	
ttc tat gga ctg gat gga tgc ttg ctg att gtg ggt gct tta gct tta Phe Tyr Gly Leu Asp Gly Cys Leu Leu Ile Val Gly Ala Leu Ala Leu	845
135 140 145	
aat ata tta gcc tgt ggc agt ctg atg aga ccc ctc caa tct tct gat Asn Ile Leu Ala Cys Gly Ser Leu Met Arg Pro Leu Gln Ser Ser Asp	893
150 155 160	
tgt cct ttg cct aaa aaa ata gct cca gaa gat cta cca gat aaa tac Cys Pro Leu Pro Lys Lys Ile Ala Pro Glu Asp Leu Pro Asp Lys Tyr	941
165 170 175	
tcc att tac aat gaa aaa gga aag aat ctg gaa gaa aac ata aac att Ser Ile Tyr Asn Glu Lys Gly Lys Asn Leu Glu Glu Asn Ile Asn Ile	989
180 185 190 195	
ctt gac aag agc tac agt agt gag gaa aaa tgc agg atc acg tta gcc Leu Asp Lys Ser Tyr Ser Ser Glu Glu Lys Cys Arg Ile Thr Leu Ala	1037
200 205 210	

Sequence Listing

aat ggt gac tgg aaa caa gac agc cta ctt cat aaa aac ccc aca gtg	1085
Asn Gly Asp Trp Lys Gln Asp Ser Leu Leu His Lys Asn Pro Thr Val	
215 220 225	
aca cac aca aaa gag cct gaa acg tac aaa aag aaa gtt gca gaa cag	1133
Thr His Thr Lys Glu Pro Glu Thr Tyr Lys Lys Lys Val Ala Glu Gln	
230 235 240	
aca tat ttt tgc aaa cag ctt gcc aag agg aag tgg cag tta tat aaa	1181
Thr Tyr Phe Cys Lys Gln Leu Ala Lys Arg Lys Trp Gln Leu Tyr Lys	
245 250 255	
aac tac tgt ggt gaa act gtg gct ctt ttt aaa aac aaa gta ttt tca	1229
Asn Tyr Cys Gly Glu Thr Val Ala Leu Phe Lys Asn Lys Val Phe Ser	
260 265 270 275	
gcc ctt ttc att gct atc tta ctc ttt gac atc gga ggg ttt cca cct	1277
Ala Leu Phe Ile Ala Ile Leu Leu Phe Asp Ile Gly Gly Phe Pro Pro	
280 285 290	
tca tta ctt atg gaa gat gta gca aga agt tca aac gtg aaa gaa gaa	1325
Ser Leu Leu Met Glu Asp Val Ala Arg Ser Ser Asn Val Lys Glu Glu	
295 300 305	
gag ttt att atg cca ctt att tcc att ata ggc att atg aca gca gtt	1373
Glu Phe Ile Met Pro Leu Ile Ser Ile Ile Gly Ile Met Thr Ala Val	
310 315 320	
ggt aaa ctg ctt tta ggg ata ctg gct gac ttc aag tgg att aat acc	1421
Gly Lys Leu Leu Leu Gly Ile Leu Ala Asp Phe Lys Trp Ile Asn Thr	
325 330 335	
ttg tat ctt tat gtt gct acc tta atc atc atg ggc cta gcc ttg tgt	1469
Leu Tyr Leu Tyr Val Ala Thr Leu Ile Ile Met Gly Leu Ala Leu Cys	
340 345 350 355	
gca att cca ttt gcc aaa agc tat gtc aca ttg gcg ttg ctt tct ggg	1517
Ala Ile Pro Phe Ala Lys Ser Tyr Val Thr Leu Ala Leu Leu Ser Gly	
360 365 370	

Sequence Listing

atc cta ggg ttt ctt act ggt aat tgg tcc atc ttt cca tat gtg acc Ile Leu Gly Phe Leu Thr Gly Asn Trp Ser Ile Phe Pro Tyr Val Thr <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 375 380 385 </div>	1565
acg aag act gtg gga att gaa aaa tta gcc cat gcc tat ggg ata tta Thr Lys Thr Val Gly Ile Glu Lys Leu Ala His Ala Tyr Gly Ile Leu <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 390 395 400 </div>	1613
atg ttc ttt gct gga ctt gga aat agc cta gga cca ccc atc gtt ggt Met Phe Phe Ala Gly Leu Gly Asn Ser Leu Gly Pro Pro Ile Val Gly <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 405 410 415 </div>	1661
tgg ttt tat gac tgg acc cag acc tat gat att gca ttt tat ttt agt Trp Phe Tyr Asp Trp Thr Gln Thr Tyr Asp Ile Ala Phe Tyr Phe Ser <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 420 425 430 435 </div>	1709
ggc ttc tgc gtc ctg ctg gga ggt ttt att ctg ctg ctg gca gcc ttg Gly Phe Cys Val Leu Leu Gly Gly Phe Ile Leu Leu Leu Ala Ala Leu <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 440 445 450 </div>	1757
ccc tct tgg gat aca tgc aac aag caa ctc ccc aag cca gct cca aca Pro Ser Trp Asp Thr Cys Asn Lys Gln Leu Pro Lys Pro Ala Pro Thr <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 455 460 465 </div>	1805
act ttc ttg tac aaa gtt gcc tct aat gtt Thr Phe Leu Tyr Lys Val Ala Ser Asn Val <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 470 475 </div>	1850
agacactatt ttgctattt tataccatat agcaacgata tttaacaga totcaagcaa 	1910
attttctaga gtcaagacta ttttctcata gcaaaatttc acaatgactg actctgaatg 	1970
aattattttt ttttttttat atatcctatt ttttatgtag tgtatgcgta gcctctatct 	2030
cgtatttttt tctattttctc ctccccacac catcaatggg actattctgt ttgctgtta 	2090
ttactagtt cttaacattg taaaaagttt gaccagcctc agaaggcttt ctctgtgtaa 	2150
agaagtataa tttctctgct gactccattt aatccactgc aaggcaccta gagagactgc 	2210

Sequence Listing

tcctatttta aaagtgatgc aagcatcatg ataagatatg tgtgaagccc actaggaaat 2270

aaatcattct cttctctatg ttgacttgc tagtaaacag aagacttcaa gccagccagg 2330

aaattaaagt ggcgactaaa acagccttaa gaattgcagt ggagcaaatt ggtcattttt 2390

taaaaaata tattttaacc tacagtcacc agttttcatt attctattta cctcactgaa 2450

gtactcgcat gttgtttggt acccactgag caactgtttc agttcctaag gtatttgctg 2510

agatgtgggt gaactccaaa tggagaagta gtcactgtag actttcttca tggttgacca 2570

ctccaacctt gctcactttt gcttcttggc catccactca gctgatgttt cctgggaagt 2630

gctaatttta cctgtttcca aattggaaac acatttctca atcattccgt tctggcaaat 2690

gggaaacatc catttgcttt gggcacagtg gggatgggct gcaagttctt gcatatcctc 2750

ccagtgaagc atttatttgc tactatcaga ttttaccact atcaaatata attcaagggc 2810

agaattaaac gtgagtgtgt gtgtgtgtgt gtgtgtgtgt gctatgcatg ctctaagtct 2870

gcatgggata tgggaatgga aaagggcaat aagaaattaa tacccttatg cagttgcatt 2930

taaccttaag aaaaatgtcc ttgggataaa ctccaatgtt taatacattg attttttttc 2990

taaagaaatg ggttttaaac ttgggtatgc atcagaattc cctatagatc tttttgaaaa 3050

tataggtacc tgggtatcac acatagaact tttaattctg ctggtgtagg ctgttgccca 3110

aacatctata attttactga gctcttcaag tgattctgat aacacagcct gg 3162

<210> 8

<211> 477

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Leu Lys Lys Ser Pro Asp Gly Gly Trp Gly Trp Val Ile Val

Sequence Listing

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20	25	30	
Val Gly Val Leu Tyr Ile Glu Trp Leu Asp Ala Phe Gly Glu Gly Lys			
35	40	45	
Gly Lys Thr Ala Trp Val Gly Ser Leu Ala Ser Gly Val Gly Leu Leu			
50	55	60	
Ala Ser Pro Val Cys Ser Leu Cys Val Ser Ser Phe Gly Ala Arg Pro			
65	70	75	80
Val Thr Ile Phe Ser Gly Phe Met Val Ala Gly Gly Leu Met Leu Ser			
85	90	95	
Ser Phe Ala Pro Asn Ile Tyr Phe Leu Phe Phe Ser Tyr Gly Ile Val			
100	105	110	
Val Gly Ser Ser Val Gly Leu Phe Ile Tyr Ala Ala Leu Gln Arg Met			
115	120	125	
Leu Val Glu Phe Tyr Gly Leu Asp Gly Cys Leu Leu Ile Val Gly Ala			
130	135	140	
Leu Ala Leu Asn Ile Leu Ala Cys Gly Ser Leu Met Arg Pro Leu Gln			
145	150	155	160
Ser Ser Asp Cys Pro Leu Pro Lys Lys Ile Ala Pro Glu Asp Leu Pro			
165	170	175	
Asp Lys Tyr Ser Ile Tyr Asn Glu Lys Gly Lys Asn Leu Glu Glu Asn			
180	185	190	
Ile Asn Ile Leu Asp Lys Ser Tyr Ser Ser Glu Glu Lys Cys Arg Ile			
195	200	205	
Thr Leu Ala Asn Gly Asp Trp Lys Gln Asp Ser Leu Leu His Lys Asn			
210	215	220	

Sequence Listing

Pro Thr Val Thr His Thr Lys Glu Pro Glu Thr Tyr Lys Lys Lys Val
225 230 235 240

Ala Glu Gln Thr Tyr Phe Cys Lys Gln Leu Ala Lys Arg Lys Trp Gln
245 250 255

Leu Tyr Lys Asn Tyr Cys Gly Glu Thr Val Ala Leu Phe Lys Asn Lys
260 265 270

Val Phe Ser Ala Leu Phe Ile Ala Ile Leu Leu Phe Asp Ile Gly Gly
275 280 285

Phe Pro Pro Ser Leu Leu Met Glu Asp Val Ala Arg Ser Ser Asn Val
290 295 300

Lys Glu Glu Glu Phe Ile Met Pro Leu Ile Ser Ile Ile Gly Ile Met
305 310 315 320

Thr Ala Val Gly Lys Leu Leu Leu Gly Ile Leu Ala Asp Phe Lys Trp
325 330 335

Ile Asn Thr Leu Tyr Leu Tyr Val Ala Thr Leu Ile Ile Met Gly Leu
340 345 350

Ala Leu Cys Ala Ile Pro Phe Ala Lys Ser Tyr Val Thr Leu Ala Leu
355 360 365

Leu Ser Gly Ile Leu Gly Phe Leu Thr Gly Asn Trp Ser Ile Phe Pro
370 375 380

Tyr Val Thr Thr Lys Thr Val Gly Ile Glu Lys Leu Ala His Ala Tyr
385 390 395 400

Gly Ile Leu Met Phe Phe Ala Gly Leu Gly Asn Ser Leu Gly Pro Pro
405 410 415

Ile Val Gly Trp Phe Tyr Asp Trp Thr Gln Thr Tyr Asp Ile Ala Phe
420 425 430

Sequence Listing

Tyr Phe Ser Gly Phe Cys Val Leu Leu Gly Gly Phe Ile Leu Leu Leu
 435 440 445

Ala Ala Leu Pro Ser Trp Asp Thr Cys Asn Lys Gln Leu Pro Lys Pro
 450 455 460

Ala Pro Thr Thr Phe Leu Tyr Lys Val Ala Ser Asn Val
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<210> 9
 <211> 4891
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (89) .. (1150)
 <223> Clone LBFL131

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tgctggagag tgagcagccc tagcaggg atg gac atg atg ctg ttg gtg cag 112
 Met Asp Met Met Leu Leu Val Gln
 1 5

ggg gct tgt tgc tcg aac cag tgg ctg gcg gcg gtg ctc ctc agc ctg 160
 Gly Ala Cys Cys Ser Asn Gln Trp Leu Ala Ala Val Leu Leu Ser Leu
 10 15 20

tgc tgc ctg cta ccc tcc tgc ctc ccg gct gga cag agt gtg gac ttc 208
 Cys Cys Leu Leu Pro Ser Cys Leu Pro Ala Gly Gln Ser Val Asp Phe
 25 30 35 40

ccc tgg gcg gcc gtg gac aac atg atg gtc aga aaa ggg gac acg gcg 256
 Pro Trp Ala Ala Val Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala
 45 50 55

Sequence Listing

gtg ctt agg tgt tat ttg gaa gat gga gct tca aag ggt gcc tgg ctg	304
Val Leu Arg Cys Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu	
60 65 70	
aac cgg tca agt att att ttt gcg gga ggt gat aag tgg tca gtg gat	352
Asn Arg Ser Ser Ile Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp	
75 80 85	
cct cga gtt tca att tca aca ttg aat aaa agg gac tac agc ctc cag	400
Pro Arg Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln	
90 95 100	
ata cag aat gta gat gtg aca gat gat ggc cca tac acg tgt tct gtt	448
Ile Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val	
105 110 115 120	
cag act caa cat aca ccc aga aca atg cag gtg cat cta act gtg caa	496
Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln	
125 130 135	
gtt cct cct aag ata tat gac atc tca aat gat atg acc gtc aat gaa	544
Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu	
140 145 150	
gga acc aac gtc act ctt act tgt ttg gcc act ggg aaa cca gag cct	592
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu Pro	
155 160 165	
tcc att tct tgg cga cac atc tcc cca tca gcg aaa cca ttt gaa aat	640
Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe Glu Asn	
170 175 180	
gga caa tat ttg gac att tat gga att aca agg gac cag gct ggg gaa	688
Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln Ala Gly Glu	
185 190 195 200	
tat gaa tgc agt gcg gaa aat gat gtg tca ttc cca gat gtg agg aaa	736
Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser Phe Pro Asp Val Arg Lys	
205 210 215	

Sequence Listing

gta aaa gtt gtt gtc aac ttt gct cct act att cag gaa att aaa tct Val Lys Val Val Val Asn Phe Ala Pro Thr Ile Gln Glu Ile Lys Ser 220 225 230	784
ggc acc gtg acc ccc gga cgc agt ggc ctg ata aga tgt gaa ggt gca Gly Thr Val Thr Pro Gly Arg Ser Gly Leu Ile Arg Cys Glu Gly Ala 235 240 245	832
ggt gtg ccg cct cca gcc ttt gaa tgg tac aaa gga gag aag aag ctc Gly Val Pro Pro Pro Ala Phe Glu Trp Tyr Lys Gly Glu Lys Lys Leu 250 255 260	880
ttc aat ggc caa caa gga att att att caa aat ttt agc aca aga tcc Phe Asn Gly Gln Gln Gly Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser 265 270 275 280	928
att ctc act gtt acc aac gtg aca cag gag cac ttc ggc aat tat act Ile Leu Thr Val Thr Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr 285 290 295	976
tgt gtg gct gcc aac aag cta ggc aca acc aat gcg agc ctg cct ctt Cys Val Ala Ala Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu 300 305 310	1024
aac cct cca agt aca gcc cag tat gga att acc ggg agc gct gat gtt Asn Pro Pro Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val 315 320 325	1072
ctt ttc tcc tgc tgg tac ctt gtg ttg aca ctg tcc tct ttc acc agc Leu Phe Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser 330 335 340	1120
ata ttc tac ctg aag aat gcc att cta caa taaattcaaa gaccataaa Ile Phe Tyr Leu Lys Asn Ala Ile Leu Gln 345 350	1170
aggcttttaa ggattctctg aaagtgctga tggctggatc caatctggta cagtttgtaa 	1230
aaagcagcgt gggatataat cagcagtgct tacatgggga tgatcgcctt ctgtagaatt 	1290

Sequence Listing

gctcattatg taaatacttt aattctactc ttttttgatt agctacatta ccttgtgaag	1350
cagtacacat tgtccttttt ttaagacgtg aaagctctga aattactttt agaggatatt	1410
aattgtgatt tcatgtttgt aatctacaac ttttcaaaag cattcagtca tggctctgcta	1470
ggttgcaggc tgtagtttac aaaaacgaat attgcagtga atatgtgatt ctttaaggct	1530
gcaatacaag cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca	1590
tttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt cttcaaaata	1650
taacacatat ctagattttt ctgctcgcat gatattcagg ttcaggaat gagccttgta	1710
atataactgg ctgtgcagct ctgcttctct ttcctgtaag ttcagcatgg gtgtgccttc	1770
atacaataat atttttctct ttgtctcaa ctaatataaa atgttttgct aaatcttaca	1830
atttgaaagt aaaaataaac cagagtgatc aagttaaacc atacactatc tctaagtaac	1890
gaaggagcta ttggactgta aaaatctctt cctgcactga caatgggggt tgagaatttt	1950
gccccacact aactcagttc ttgtgatgag agacaattta ataacagtat agtaaata	2010
ccatatgatt tctttagttg tagctaaatg ttagatccac cgtgggaaat tattcccttt	2070
aaaatgacag cacagtccac tcaaaggatt gcctagcaat acagcatctt ttcctttcac	2130
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atattacaag agttggtaag cgctcatcat taattttatt ttgtggcagc taagttagta	2250
tgacagaggc agtgctcctg tggacaggag catthttgcat atttccatc tgaaagtatc	2310
actcagttga tagtctggaa tgcatgttat atattttaaa acttcacaaa tatattataa	2370
caaacattct atatcggtat gtagcagacc aatctctaaa atagctaatt cttcaataaa	2430
atctttctat atagccattt cagtgcacaa aagtaaaatc aaaaaagacc atcctttatt	2490

Sequence Listing

tttccttaca tgatatatgt aagatgcat caaataaaga caaaacacca gtgatgagaa	2550
tatcttaaga taagtaatta tcaaattatt gtgaatgtta aattatttct actataaaga	2610
agcaaaacta catttttgaa ggaaaatgct gttactctaa cattaattta caggaatagt	2670
ttgatgggtt cactctttac taaagaaagg ccatcacctt gaaagccatt ttacagggtt	2730
gatgaagtta ccaatttcag tacacctaaa tttctacaaa tagtcccctt ttacaagttg	2790
taacaacaaa gaccctataa taaaattaga tacaagaaat tttgcagtgg ttatacatat	2850
ttgagatatc tagtatgttg ccctagcagg gatggcttaa aaactgtgat ttttttctt	2910
caagtaaac ttagtcccaa agtacatcat aaatcaattt taactagaaa aatgaatctt	2970
aaatgagggg acataagtat actctttcca caaaatggca ataataaggc ataaagctag	3030
taaatctact aactgtaata aatgtatgac attattttga ttgatacatt aaaaaagagt	3090
ttttagaaca aatatggcat ttaactttat tatttatttg cttttaagaa atattctttg	3150
tggaattgtt gaataaacta taaaatatta ttttgatttg cagctttaaa gtggcacact	3210
ccataataat ctacctacta gaaatagtgg tgctaccaca aaaaatgtta accatcagta	3270
ccattgtttg ggagaaagaa acaggtcaag aatgcatatt attcagtgc cgctttccta	3330
gagttaaaat acctcctctt tgtaagggtt gtaggtaaat tgaggtataa actatggatg	3390
aaccaaataa ttagttcaaa gtgttgatcat gattccaaat ttgtggagtc tgggtgtttt	3450
accatagaat gtgacagaag tacagtcata gctcagtagc tatatgtatt tgcctttatg	3510
ttagaagaga ctttcttgag tgacattttt aaatagagga ggtattcact atgttttct	3570
gtatcacagc agcattccta gtccttaggc cctcggacag agtgaaatca tgagtattta	3630
tgagttcaat attgtcaaat aaggctacag tatttgcttt tttgtgtgaa tgtattgcat	3690

Sequence Listing

ataatgttca agtagatgat ttacattta tggacatata aaacgtctga ttacccatt	3750
ttatcagtcc tgactgtaca agattgttgc aatttcagaa tagcagtttt ataaattgat	3810
ttatctttta atctataaca atttgtgtta gctgttcatt tcaggattat attttctaca	3870
agttccactt gtgggactcc ttttgttgcc cctatttttt tttaaagaag gaagaaagaa	3930
aatgagtag cagtttaaaa atgagaatgg agagaaaaga aaaagaatga aaaggaaagg	3990
cagtaaagag ggaaaaaaaa ggaaggatgg aaggaatgaa ggaagggaagg gaggaagggg	4050
agaaggtagg aagaaagaaa ggatgagagg gaaggaagaa tcagagtatt agggtagtta	4110
acttacacat ttgcattctt agttatactg caagtgggtg aactatgttt ttcaatgatc	4170
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aaaaagtact gcccaagtta tagtaatgtg ggtgtttttg agacactaaa agatttgaga	4290
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gcttcatcat aacatttaag ctatatctag aaagtagact ggagaactga gaaaattacc	4410
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aacaattgtt aatttatcca ttgtgcttag ctttgtgaca cagccaaaag ttacctattt	4590
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ctgtctttta gtaaacaatc atatttcata acctgatgta aaatatgttg tactgtttcc	4830
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Sequence Listing

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4891

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 10

Met Asp Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp
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Leu Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu
20 25 30

Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn Met
35 40 45

Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu Glu Asp
50 55 60

Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile Ile Phe Ala
65 70 75 80

Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser Ile Ser Thr Leu
85 90 95

Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn Val Asp Val Thr Asp
100 105 110

Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr Gln His Thr Pro Arg Thr
115 120 125

Met Gln Val His Leu Thr Val Gln Val Pro Pro Lys Ile Tyr Asp Ile
130 135 140

Ser Asn Asp Met Thr Val Asn Glu Gly Thr Asn Val Thr Leu Thr Cys
145 150 155 160

Leu Ala Thr Gly Lys Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser

Sequence Listing

165	170	175
Pro Ser Ala Lys Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly		
180	185	190
Ile Thr Arg Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp		
195	200	205
Val Ser Phe Pro Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala		
210	215	220
Pro Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser		
225	230	235
		240
Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu		
245	250	255
Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile		
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val Thr		
275	280	285
Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly		
290	295	300
Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr Ala Gln Tyr		
305	310	315
		320
Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys Trp Tyr Leu Val		
325	330	335
Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr Leu Lys Asn Ala Ile		
340	345	350
Leu Gln		

<210> 11

Sequence Listing

<211> 3098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (223) .. (1569)
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 gctggcgccct ggtccctcc gggtttcggt tcccgccggc gcctggctcc cgccaggttt 180
 cgtttccgag gcggggccga gggcggcgtc gctgaggcgc cc atg gcc ttc 231
 Met Ala Phe
 1
 gcc cgc cgg ctc ctg cgc ggg cca ctg tcg ggg ccg ctg ctc ggg cgg 279
 Ala Arg Arg Leu Leu Arg Gly Pro Leu Ser Gly Pro Leu Leu Gly Arg
 5 10 15
 cgc ggg gtc tgc gct ggg gcc atg gct ccg ccg cgc cgc ttc gtc ctg 327
 Arg Gly Val Cys Ala Gly Ala Met Ala Pro Pro Arg Arg Phe Val Leu
 20 25 30 35
 gag ctt ccc gac tgc acc ctg gct cac ttc gcc cta ggc gcc gac gcc 375
 Glu Leu Pro Asp Cys Thr Leu Ala His Phe Ala Leu Gly Ala Asp Ala
 40 45 50
 ccc ggc gac gca gac gcc ccc gac ccc cgc ctg gcg gcg ctg ctg ggg 423
 Pro Gly Asp Ala Asp Ala Pro Asp Pro Arg Leu Ala Ala Leu Leu Gly
 55 60 65
 ccc ccg gag cgc agc tac tcg ctg tgc gtg ccc gtg acc ccg gac gcc 471
 Pro Pro Glu Arg Ser Tyr Ser Leu Cys Val Pro Val Thr Pro Asp Ala
 70 75 80

Sequence Listing

ggc tgc ggg gcc cgg gtc cgg gcg gcg cgg ctg cac cag cgc ctg ctg	519
Gly Cys Gly Ala Arg Val Arg Ala Ala Arg Leu His Gln Arg Leu Leu	
85 90 95	
cac cag ctg cgc cgc ggc ccc ttc cag cgg tgc cag ctg ctc agg ctg	567
His Gln Leu Arg Arg Gly Pro Phe Gln Arg Cys Gln Leu Leu Arg Leu	
100 105 110 115	
ctc tgc tac tgc ccg ggc ggc cag gcc ggc ggc gca cag caa ggc ttc	615
Leu Cys Tyr Cys Pro Gly Gly Gln Ala Gly Gly Ala Gln Gln Gly Phe	
120 125 130	
ctg ctg cgc gac ccc ctg gat gac cct gac acc cgg caa gcg ctg ctc	663
Leu Leu Arg Asp Pro Leu Asp Asp Pro Asp Thr Arg Gln Ala Leu Leu	
135 140 145	
gag ctg ctg ggc gcc tgc cag gag gca cca cgc ccg cac ttg ggc gag	711
Glu Leu Leu Gly Ala Cys Gln Glu Ala Pro Arg Pro His Leu Gly Glu	
150 155 160	
ttc gag gcc gac ccg cgc ggc cag ctg tgg cag cgc ctc tgg gag gtg	759
Phe Glu Ala Asp Pro Arg Gly Gln Leu Trp Gln Arg Leu Trp Glu Val	
165 170 175	
caa gac ggc agg cgg ctg cag gtg ggc tgc gca cag gtc gtg ccc gtc	807
Gln Asp Gly Arg Arg Leu Gln Val Gly Cys Ala Gln Val Val Pro Val	
180 185 190 195	
ccg gag ccc ccg ctg cac ccg gtg gtg cca gac ttg ccc agt tcc gtg	855
Pro Glu Pro Pro Leu His Pro Val Val Pro Asp Leu Pro Ser Ser Val	
200 205 210	
gtc ttc ccg gac cgg gaa gcc gcc cgg gcc gtt ttg gag gag tgt acc	903
Val Phe Pro Asp Arg Glu Ala Ala Arg Ala Val Leu Glu Glu Cys Thr	
215 220 225	
tcc ttt att cct gaa gcc cgg gca gtg ctt gac ctg gtc gac cag tgc	951
Ser Phe Ile Pro Glu Ala Arg Ala Val Leu Asp Leu Val Asp Gln Cys	
230 235 240	

Sequence Listing

cca aaa cag atc cag aaa gga aag ttc cag gtt gtt gcc atc gaa gga	999
Pro Lys Gln Ile Gln Lys Gly Lys Phe Gln Val Val Ala Ile Glu Gly	
245 250 255	
ctg gat gcc acg ggt aaa acc acg gtg acc cag tca gtg gca gat tca	1047
Leu Asp Ala Thr Gly Lys Thr Thr Val Thr Gln Ser Val Ala Asp Ser	
260 265 270 275	
ctt aag gct gtc ctc tta aag tca cca ccc tct tgc att ggc cag tgg	1095
Leu Lys Ala Val Leu Leu Lys Ser Pro Pro Ser Cys Ile Gly Gln Trp	
280 285 290	
agg aag atc ttt gat gat gaa cca act atc att aga aga gct ttt tac	1143
Arg Lys Ile Phe Asp Asp Glu Pro Thr Ile Ile Arg Arg Ala Phe Tyr	
295 300 305	
tct ttg ggc aat tat att gtg gcc tcc gaa ata gct aaa gaa tct gcc	1191
Ser Leu Gly Asn Tyr Ile Val Ala Ser Glu Ile Ala Lys Glu Ser Ala	
310 315 320	
aaa tct cct gtg att gta gac agg tac tgg cac agc acg gcc acc tat	1239
Lys Ser Pro Val Ile Val Asp Arg Tyr Trp His Ser Thr Ala Thr Tyr	
325 330 335	
gct ata gcc act gag gtg agt ggg ggt ctc cag cac ctg ccc cca gcc	1287
Ala Ile Ala Thr Glu Val Ser Gly Gly Leu Gln His Leu Pro Pro Ala	
340 345 350 355	
cat cac cct gtg tac cag tgg cca gag gac ctg ctc aaa cct gac ctt	1335
His His Pro Val Tyr Gln Trp Pro Glu Asp Leu Leu Lys Pro Asp Leu	
360 365 370	
atc ctg ctg ctc act gtg agt cct gag gag agg ttg cag agg ctg cag	1383
Ile Leu Leu Leu Thr Val Ser Pro Glu Glu Arg Leu Gln Arg Leu Gln	
375 380 385	
ggc cgg ggc atg gag aag acc agg gaa gaa gca gaa ctt gag gcc aac	1431
Gly Arg Gly Met Glu Lys Thr Arg Glu Glu Ala Glu Leu Glu Ala Asn	
390 395 400	

Sequence Listing

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agt gtg ttt cgt caa aag gta gaa atg tcc tac cag cgg atg gag aat      1479
Ser Val Phe Arg Gln Lys Val Glu Met Ser Tyr Gln Arg Met Glu Asn
    405                410                415

cct ggc tgc cat gtg gtt gat gcc agc ccc tcc aga gaa agg gtc ctg      1527
Pro Gly Cys His Val Val Asp Ala Ser Pro Ser Arg Glu Arg Val Leu
    420                425                430                435

cag acg gta tta agc cta atc cag aat agt ttt agt gaa ccg              t      1570
Gln Thr Val Leu Ser Leu Ile Gln Asn Ser Phe Ser Glu Pro
    440                445

agttactctg gccaggtgcc acgtctaact agattagatg ttgtttgaaa catctacatc      1630

caccatttgt tatgcagtgt tcccaaattt ctgttctaca agcatgttgt gtggcagaaa      1690

actggagacc aggcatttta attttacttc agccatcgta ccctcttctg actgatggac      1750

ccgtcatcac aaagggccct ctcatcatgt tccagtgaga .ggccagcgat tgctttcttc      1810

ctggcatagt aaacattttc ttggaacata tgtttcactt aatcactacc aaatatctgg      1870

aagacctgtc ttactcagac agcaccaggt gtacagaagc agcagacaag atcttccaga      1930

tcagcaggga gaccccgag cctctgcttc tctacactg gcatgctgat gagatcgtga      1990

catgcccaca ttggcttctt ccacatctgg ttgcactcgt catgatgggc tcgctgcatc      2050

tccctcagtc ccaaattcta gagccaagtg ttcttgcaga ggctgtctat gtgtcttggc      2110

tgcccaagga cactcctgca gagccatttt tgggtaagga acacttaca agaaggcatt      2170

gatcttgtgt ctgaggctca gagccctttt gataggcttc tgagtcatat ataaagacat      2230

tcaagccaag atgctccaac tgcaaata ccaaccttct ctgaattata ttttgcttat      2290

ttatatttct tttctttttt tctaaagtat ggctctgaat agaatgcaca ttttccattg      2350

aactggatgc atttcattta gccaatccag taatttat atattaatct atacaatatg      2410

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Sequence Listing

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tttcctcagc ataggagcta tgattcatta attaaaagtg gagtcaaaac gctaaatgca      2470
atgtttgttg tgtattttca ttacacaaac ttaatttgtc ttgttaaata agtacagtgg      2530
atcttgaggt gggatttctt ggtaaattat cttgcacttg aatgtctcat gattacatat      2590
gaaatcgctt tgacatatct ttagacagaa aaaagtagct gagtgagggg gaaattatag      2650
agctgtgtga ctttagggag taggttgaac caggtgatta cctaaaattc cttccagttc      2710
aaaggcagat aaatctgtaa attattttat cctatctacc atttcttaag aagacattac      2770
tccaaaataa ttaaatttaa ggctttatca ggtctgcata tagaatctta aattctaata      2830
aagtttcatg ttaatgtcat aggattttta aaagagctat aggtaatttc tatataatat      2890
gtgtatatta aaatgtaatt gatttcagtt gaaagtattt taaagctgat aaatagcatt      2950
agggttcttt gcaatgtggt atctagctgt attattgggt ttatttactt taaacatttt      3010
gaaaagctta tactggcagc ctagaaaaac aaacaattaa tgtatcttta tgcacctggc      3070
acatgaataa actttgctgt ggtttact      3098

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<210> 12

<211> 449

<212> PRT

<213> Homo sapiens

<400> 12

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Met Ala Phe Ala Arg Arg Leu Leu Arg Gly Pro Leu Ser Gly Pro Leu
  1              5              10              15

```

```

Leu Gly Arg Arg Gly Val Cys Ala Gly Ala Met Ala Pro Pro Arg Arg
      20              25              30

```

```

Phe Val Leu Glu Leu Pro Asp Cys Thr Leu Ala His Phe Ala Leu Gly
      35              40              45

```

Sequence Listing

Ala Asp Ala Pro Gly Asp Ala Asp Ala Pro Asp Pro Arg Leu Ala Ala
50 55 60

Leu Leu Gly Pro Pro Glu Arg Ser Tyr Ser Leu Cys Val Pro Val Thr
65 70 75 80

Pro Asp Ala Gly Cys Gly Ala Arg Val Arg Ala Ala Arg Leu His Gln
85 90 95

Arg Leu Leu His Gln Leu Arg Arg Gly Pro Phe Gln Arg Cys Gln Leu
100 105 110

Leu Arg Leu Leu Cys Tyr Cys Pro Gly Gly Gln Ala Gly Gly Ala Gln
115 120 125

Gln Gly Phe Leu Leu Arg Asp Pro Leu Asp Asp Pro Asp Thr Arg Gln
130 135 140

Ala Leu Leu Glu Leu Leu Gly Ala Cys Gln Glu Ala Pro Arg Pro His
145 150 155 160

Leu Gly Glu Phe Glu Ala Asp Pro Arg Gly Gln Leu Trp Gln Arg Leu
165 170 175

Trp Glu Val Gln Asp Gly Arg Arg Leu Gln Val Gly Cys Ala Gln Val
180 185 190

Val Pro Val Pro Glu Pro Pro Leu His Pro Val Val Pro Asp Leu Pro
195 200 205

Ser Ser Val Val Phe Pro Asp Arg Glu Ala Ala Arg Ala Val Leu Glu
210 215 220

Glu Cys Thr Ser Phe Ile Pro Glu Ala Arg Ala Val Leu Asp Leu Val
225 230 235 240

Asp Gln Cys Pro Lys Gln Ile Gln Lys Gly Lys Phe Gln Val Val Ala
245 250 255

Sequence Listing

Ile Glu Gly Leu Asp Ala Thr Gly Lys Thr Thr Val Thr Gln Ser Val
260 265 270

Ala Asp Ser Leu Lys Ala Val Leu Leu Lys Ser Pro Pro Ser Cys Ile
275 280 285

Gly Gln Trp Arg Lys Ile Phe Asp Asp Glu Pro Thr Ile Ile Arg Arg
290 295 300

Ala Phe Tyr Ser Leu Gly Asn Tyr Ile Val Ala Ser Glu Ile Ala Lys
305 310 315 320

Glu Ser Ala Lys Ser Pro Val Ile Val Asp Arg Tyr Trp His Ser Thr
325 330 335

Ala Thr Tyr Ala Ile Ala Thr Glu Val Ser Gly Gly Leu Gln His Leu
340 345 350

Pro Pro Ala His His Pro Val Tyr Gln Trp Pro Glu Asp Leu Leu Lys
355 360 365

Pro Asp Leu Ile Leu Leu Leu Thr Val Ser Pro Glu Glu Arg Leu Gln
370 375 380

Arg Leu Gln Gly Arg Gly Met Glu Lys Thr Arg Glu Glu Ala Glu Leu
385 390 395 400

Glu Ala Asn Ser Val Phe Arg Gln Lys Val Glu Met Ser Tyr Gln Arg
405 410 415

Met Glu Asn Pro Gly Cys His Val Val Asp Ala Ser Pro Ser Arg Glu
420 425 430

Arg Val Leu Gln Thr Val Leu Ser Leu Ile Gln Asn Ser Phe Ser Glu
435 440 445

Pro

Sequence Listing

<210> 13
 <211> 1893
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (418)..(1392)
 <223> LBFL167 Clone #20

<400> 13
 agtccagctg ccgttaggcg ctgggatagt cgcacgctgg atgcatctac gtccgccgag 60
 cccctggggc gaagaggccg cgtccgcctt catttggtggc cgggtgcttcg cccctgacc 120
 cttcgcccc aaagaccagc tctaactga gcgcctcggc cgccctgccc cagcctcgta 180
 cagccgcca gcctcgcca gccggtgtcc ggagaccctc gggccgtgtc catttggtgg 240
 caaagccagc ggggcaggct tggccagagt gcaccactcg gcgccgtccc aggcccgacg 300
 ctctggggcg gcccggaacc ccaggttcgc ggcccgtgtt tccgaccggc ggagggggct 360
 cagcgccccg atccacgga agcgcgctcg gaggggtggg acccgccgg accggag 417
 atg gcg ccg cca gcg ggc ggg gcg gcg gcg gcg gcc tcg gac ttg ggc 465
 Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ser Asp Leu Gly
 1 5 10 15
 tcc gcc gca gtg ctc ttg gct gtg cac gcc gcg gtg agg ccg ctg ggc 513
 Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly
 20 25 30
 gcc ggg cca gac gcc gag gca cag ctg cgg agg ctg cag ctg agc gcg 561
 Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala
 35 40 45
 gac cct gag cgg cct ggg cgc ttc cgg ctg gag ctg ctg ggc gcg gga 609
 Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly

Sequence Listing

50	55	60	
cct ggg gcg gtt aat ttg gag tgg ccc ctg gag tca gtt tcc tac acc			657
Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr			
65	70	75	80
atc cga ggc ccc acc cag cac gag cta cag cct cca cca gga ggg cct			705
Ile Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro			
85	90	95	
gga acc ctc agc ctg cac ttc ctc aac cct cag gaa gct cag cgg tgg			753
Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp			
100	105	110	
gca gtc cta gtc cga ggt gcc acc gtg gaa gga cag aat ggc agc aag			801
Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys			
115	120	125	
agc aac tca cca cca gcc ttg ggc cca gaa gca tgc cct gtc tcc ctg			849
Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu			
130	135	140	
acc agt ccc ccg gaa gcc tcc aca ctc aag ggc cct cca cct gag gca			897
Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala			
145	150	155	160
gat ctt cct agg agc cct gga aac ttg acg gag aga gaa gag ctg gca			945
Asp Leu Pro Arg Ser Pro Gly Asn Leu Thr Glu Arg Glu Glu Leu Ala			
165	170	175	
agg agc ctg gcc cgg gct att gca ggt gga gac gag aag ggg gca gcc			993
Ily Ser Leu Ala Arg Ala Ile Ala Gly Gly Asp Glu Lys Gly Ala Ala			
180	185	190	
aaa gtg gca gcc gtc ctg gcc cag cat cgt gtg gcc ctg agt gtt cag			1041
Iln Val Ala Ala Val Leu Ala Gln His Arg Val Ala Leu Ser Val Gln			
195	200	205	
tt cag gag gcc tgc ttc cca cct ggc ccc atc agg ctg cag gtc aca			1089
eu Gln Glu Ala Cys Phe Pro Pro Gly Pro Ile Arg Leu Gln Val Thr			

Sequence Listing

210	215	220	
ctt gaa gac gct gcc tot gcc gca tcc gcc gcg tcc tct gca cac gtt			1137
Leu Glu Asp Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala His Val			
225	230	235	240
gcc ctg cag gtc cac ccc cac tgc act gtt gca gct ctc cag gag cag			1185
Ala Leu Gln Val His Pro His Cys Thr Val Ala Ala Leu Gln Glu Gln			
245	250	255	
gtg ttc tca gag ctc ggt ttc ccg cca gcc gtg caa cgc tgg gtc atc			1233
Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val Gln Arg Trp Val Ile			
260	265	270	
gga cgg tgc ctg tgt gtg cct gag cgc agc ctt gcc tct tac ggg gtt			1281
Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu Ala Ser Tyr Gly Val			
275	280	285	
cgg cag gat ggg gac cct gct ttc ctc tac ttg ctg tca gct cct cga			1329
Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg			
290	295	300	
jaa gcc cca ggt cag tcc tcg atg ggg gtg ggg tgt ggg agg tgg ggt			1377
flu Ala Pro Gly Gln Ser Ser Met Gly Val Gly Cys Gly Arg Trp Gly			
305	310	315	320
jca gcc cca cag tcc	tgagctcc accccctcag	ccacaggacc tagccctcag	1430
ala Ala Pro Gln Ser			
325			
:acccccaga agatggacgg ggaacttgga cgcttgtttc cccatcatt ggggctaccc			1490
:caggccccc agccagctgc ctccagcctg cccagtcac tccagcccag ctggtcctgt			1550
:cttcctgca cttcatcaa tgccccagac cgccctggct gtgagatgtg tagcaccag			1610
.ggccctgca ctggggaccc ccttgctgca gcttcacact agcagccacc agaggtacca			1670
'aggtggcac aggcagggga ggtggggggc cagggcagaa tccacaggaa tgaccagct			1730

Sequence Listing

cctccccac aggttacaag gggagagtgg cccttcctc acaagtccga catctccagg 1790

ccccactga actccgggga cctctactga ctgcttgctg ggacagtcac cagggttggg 1850

gggaagggcc acaaaatgaa accattaaag acccttaaga gcc 1893

<210> 14

<211> 325

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ser Asp Leu Gly
1 5 10 15

Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly
20 25 30

Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala
35 40 45

Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly
50 55 60

Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr
65 70 75 80

Gle Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro
85 90 95

Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp
100 105 110

Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys
115 120 125

Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu
130 135 140

Sequence Listing

Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala
145 150 155 160

Asp Leu Pro Arg Ser Pro Gly Asn Leu Thr Glu Arg Glu Glu Leu Ala
165 170 175

Gly Ser Leu Ala Arg Ala Ile Ala Gly Gly Asp Glu Lys Gly Ala Ala
180 185 190

Gln Val Ala Ala Val Leu Ala Gln His Arg Val Ala Leu Ser Val Gln
195 200 205

Leu Gln Glu Ala Cys Phe Pro Pro Gly Pro Ile Arg Leu Gln Val Thr
210 215 220

Leu Glu Asp Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala His Val
225 230 235 240

Ala Leu Gln Val His Pro His Cys Thr Val Ala Ala Leu Gln Glu Gln
245 250 255

Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val Gln Arg Trp Val Ile
260 265 270

Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu Ala Ser Tyr Gly Val
275 280 285

Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg
290 295 300

Glu Ala Pro Gly Gln Ser Ser Met Gly Val Gly Cys Gly Arg Trp Gly
305 310 315 320

Ala Ala Pro Gln Ser
325

<210> 15

<211> 1597

<212> DNA

Sequence Listing

<213> Homo sapiens

<220>

<221> CDS

<222> (271) .. (1431)

<223> LBFL167 Clone #46

<400> 15

gtgagcgcct cggccgcct gccccagcct cgtacacgcc gccagctcgc ccagccggtg 60

tccggagacc ctccggccgt gtccatttgt gggcaaagcc agcggggcag gcttggccag 120

agtgcaccac tcggcgccgt cccaggcccg acgctctggg cgcgcccgga accccaggtt 180

cgcggcccggt gtttccgacc ggcggagggg gctcagcggc ccgatccac ggaagcgcgc 240

tcggaggggt gggacccggc cggaccggag atg gcg ccg cca gcg ggc ggg gcg 294

Met Ala Pro Pro Ala Gly Gly Ala

1

5

gcg gcg gcg gcc tcg gac ttg ggc tcc gcc gca gtg ctc ttg gct gtg 342

Ala Ala Ala Ala Ser Asp Leu Gly Ser Ala Ala Val Leu Leu Ala Val

10

15

20

cac gcc gcg gtg agg ccg ctg ggc gcc ggg cca gac gcc gag gca cag 390

His Ala Ala Val Arg Pro Leu Gly Ala Gly Pro Asp Ala Glu Ala Gln

25

30

35

40

ctg cgg agg ctg cag ctg agc gcg gac cct gag agg cct ggg cgc ttc 438

Leu Arg Arg Leu Gln Leu Ser Ala Asp Pro Glu Arg Pro Gly Arg Phe

45

50

55

cgg ctg gag ctg ctg ggc gcg gga cct ggg gcg gtt aat ttg gag tgg 486

Arg Leu Glu Leu Leu Gly Ala Gly Pro Gly Ala Val Asn Leu Glu Trp

60

65

70

cgc ctg gag tca gtt tcc tac acc atc cga ggc ccc acc cag cac gag 534

Pro Leu Glu Ser Val Ser Tyr Thr Ile Arg Gly Pro Thr Gln His Glu

75

80

85

Sequence Listing

cta cag cct cca cca gga ggg cct gga acc ctc agc ctg cac ttc ctc Leu Gln Pro Pro Pro Gly Gly Pro Gly Thr Leu Ser Leu His Phe Leu 90 95 100	582
aac cct cag gaa gct cag cgg tgg gca gtc cta gtc cga ggt gcc acc Asn Pro Gln Glu Ala Gln Arg Trp Ala Val Leu Val Arg Gly Ala Thr 105 110 115 120	630
gtg gaa gga cag aat ggc agc aag agc aac tca cca cca gcc ttg ggc Val Glu Gly Gln Asn Gly Ser Lys Ser Asn Ser Pro Pro Ala Leu Gly 125 130 135	678
cca gaa gca tgc cct gtc tcc ctg ccc agt ccc ccg gaa gcc tcc aca Pro Glu Ala Cys Pro Val Ser Leu Pro Ser Pro Pro Glu Ala Ser Thr 140 145 150	726
ctc aag ggc cct cca cct gag gca gat ctt cct agg agc cct gga aac Leu Lys Gly Pro Pro Pro Glu Ala Asp Leu Pro Arg Ser Pro Gly Asn 155 160 165	774
ctg acg gag aga gaa gag ctg gca ggg agc ctg gcc cgg gct att gca Leu Thr Glu Arg Glu Glu Leu Ala Gly Ser Leu Ala Arg Ala Ile Ala 170 175 180	822
igt gga gac gag aag ggg gca gcc caa gtg gca gcc gtc ctg gcc cag ily Gly Asp Glu Lys Gly Ala Ala Gln Val Ala Ala Val Leu Ala Gln 185 190 195 200	870
aat cgt gtg gcc ctg agt gtt cag ctt cag gag gcc tgc ttc cca cct His Arg Val Ala Leu Ser Val Gln Leu Gln Glu Ala Cys Phe Pro Pro 205 210 215	918
gc ccc atc agg ctg cag gtc aca ctt gaa gac gct gcc tct gcc gca ly Pro Ile Arg Leu Gln Val Thr Leu Glu Asp Ala Ala Ser Ala Ala 220 225 230	966
cc gcc gcg tcc tct gca cac gtt gcc ctg cag gtc cac ccc cac tgc er Ala Ala Ser Ser Ala His Val Ala Leu Gln Val His Pro His Cys 235 240 245	1014

Sequence Listing

act gtt gca gct ctc cag gag cag gtg ttc tca gag ctc ggt ttc ccg	1062
Thr Val Ala Ala Leu Gln Glu Gln Val Phe Ser Glu Leu Gly Phe Pro	
250 255 260	
cca gcc gtg caa cgc tgg gtc atc gga cgg tgc ctg tgt gtg cct gag	1110
Pro Ala Val Gln Arg Trp Val Ile Gly Arg Cys Leu Cys Val Pro Glu	
265 270 275 280	
cgc agc ctt gcc tct tac ggg gtt cgg cag gat ggg gac cct gct ttc	1158
Arg Ser Leu Ala Ser Tyr Gly Val Arg Gln Asp Gly Asp Pro Ala Phe	
285 290 295	
ctc tac ttg ctg tca gct cct cga gaa gcc cca gcc aca gga cct agc	1206
Leu Tyr Leu Leu Ser Ala Pro Arg Glu Ala Pro Ala Thr Gly Pro Ser	
300 305 310	
act cag cac ccc cag aag atg gac ggg gaa ctt gga cgc ttg ttt ccc	1254
Pro Gln His Pro Gln Lys Met Asp Gly Glu Leu Gly Arg Leu Phe Pro	
315 320 325	
cca tca ttg ggg cta ccc cca ggc ccc cag cca gct gcc tcc agc ctg	1302
Pro Ser Leu Gly Leu Pro Pro Gly Pro Gln Pro Ala Ala Ser Ser Leu	
330 335 340	
ccc agt cca ctc cag ccc agc tgg tcc tgt cct tcc tgc acc ttc atc	1350
Pro Ser Pro Leu Gln Pro Ser Trp Ser Cys Pro Ser Cys Thr Phe Ile	
345 350 355 360	
at gcc cca gac cgc cct ggc tgt gag atg tgt agc acc cag agg ccc	1398
sn Ala Pro Asp Arg Pro Gly Cys Glu Met Cys Ser Thr Gln Arg Pro	
365 370 375	
gc act tgg gac ccc ctt gct gca gct tcc acc tagcagcca ccagaggtta	1450
ys Thr Trp Asp Pro Leu Ala Ala Ala Ser Thr	
380 385	
aaggggaga gtggcccttc cctcacaagt ccgacatctc caggccccca ctgaactccg	1510
gacactcta ctgactgctt gctgggacag tcaccagggg tggggggaag ggccacaaaa	1570

Sequence Listing

tgaaaccatt aaagaccctt aagagcc

1597

<210> 16

<211> 387

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ser Asp Leu Gly
1 5 10 15

Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly
20 25 30

Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala
35 40 45

Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly
50 55 60

Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr
65 70 75 80

Ile Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro
85 90 95

Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp
100 105 110

Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys
115 120 125

Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu
130 135 140

Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala
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Sequence Listing

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Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg
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Sequence Listing

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Sequence Listing

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Sequence Listing



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INTERNATIONAL SEARCH REPORT

International application No.
PCT/KR2003/002161

A. CLASSIFICATION OF SUBJECT MATTER IPC7 C12N 15/12, C07K 14/47, C12N 15/62, C07K 16/18, A61K 48/00 According to International Patent Classification (IPC) or to both national classification and IPC																	
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC7 C12N, C07K Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) NCBI Genbank, EMBL, Swissprot, Delphion, Pubmed "IQGAP"																	
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1"> <thead> <tr> <th>Category*</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>A</td> <td>Database NCBI Genbank [on line] Accession No. AL365181, 22 Jan. 2002 Human DNA sequence from clone RP11-284F21 on chromosome 1, complete sequence</td> <td>1- 9</td> </tr> <tr> <td>A</td> <td>Jon W. Erickson et al. " Identification of an actin cytoskeletal complex that includes IQGAP and the Cdc42 GTPase" J. Biol.Chem. Vol.272 No. 26. pp24443-24447, 26 Sep.1997</td> <td>1- 33</td> </tr> <tr> <td>A</td> <td>Shinya Kuroda et al. " Identification of IQGAP as a putative target for the small GTPase, Cdc42 and Rac1" J. Biol. Chem. Vol.271 No.38 pp23363-23367, 20 Sep. 1996</td> <td>1- 33</td> </tr> <tr> <td>A</td> <td>Michael W. Briggs et al. "IQGAP1-mediated stimulation of transcriptional co-activation by beta-catenin is modulated by calmodulin", J. Biol. Chem. Vol.277 No.9 pp7453-7465, 1 Mar. 2002 Cited in the application</td> <td>1- 33</td> </tr> </tbody> </table>			Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	A	Database NCBI Genbank [on line] Accession No. AL365181, 22 Jan. 2002 Human DNA sequence from clone RP11-284F21 on chromosome 1, complete sequence	1- 9	A	Jon W. Erickson et al. " Identification of an actin cytoskeletal complex that includes IQGAP and the Cdc42 GTPase" J. Biol.Chem. Vol.272 No. 26. pp24443-24447, 26 Sep.1997	1- 33	A	Shinya Kuroda et al. " Identification of IQGAP as a putative target for the small GTPase, Cdc42 and Rac1" J. Biol. Chem. Vol.271 No.38 pp23363-23367, 20 Sep. 1996	1- 33	A	Michael W. Briggs et al. "IQGAP1-mediated stimulation of transcriptional co-activation by beta-catenin is modulated by calmodulin", J. Biol. Chem. Vol.277 No.9 pp7453-7465, 1 Mar. 2002 Cited in the application	1- 33
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<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.																	
<table border="0"> <tr> <td> * Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed </td> <td> "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family </td> </tr> </table>			* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family													
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family																
Date of the actual completion of the international search 28 JANUARY 2004 (28.01.2004)		Date of mailing of the international search report 28 JANUARY 2004 (28.01.2004)															
Name and mailing address of the ISA/KR  Korean Intellectual Property Office 920 Dunsan-dong, Seo-gu, Daejeon 302-701, Republic of Korea Facsimile No. 82-42-472-7140		Authorized officer CHO, Myung Sun Telephone No. 82-42-481-5594 															

This international Searching Authority found multiple inventions in this international application as follows:

1. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.1 and No.3, and isolated nucleic acid molecule encoding SEQ ID No.2 and No.4.

2. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.5, and isolated nucleic acid molecule encoding SEQ ID No.6.

3. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.7, and isolated nucleic acid molecule encoding SEQ ID No.8.

4. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.9, and isolated nucleic acid molecule encoding SEQ ID No.10.

5. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.11, and isolated nucleic acid molecule encoding SEQ ID No.12.

6. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.13 and No.15, and isolated nucleic acid molecule encoding SEQ ID No.14 and No.16.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/KR2003/002161

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.b of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

a. type of material

☒

a sequence listing

☐

table(s) related to the sequence listing

b. format of material

☐

in written format

☒

in computer readable form

c. time of filing/furnishing

☐

contained in the international application as filed

☒

filed together with the international application in computer readable form

☐

furnished subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/KR2003/002161

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See separate sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-33 (in part)
Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.1 and No.3, and isolated nucleic acid molecule encoding SEQ ID No.2 and No.4.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

CORRECTED VERSION

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
29 April 2004 (29.04.2004)

PCT

(10) International Publication Number
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(51) International Patent Classification⁷: **C12N 15/12**,
C07K 14/47, C12N 15/62, C07K 16/18, A61K 48/00

Diego, CA 92122 (US). **YANG, Doo Seok** [KR/US]; 3937
Nobel Drive, #216, San Diego, CA 92122 (US).

(21) International Application Number:
PCT/KR2003/002161

(74) Agent: **SOHN, Chang Kyu**; 4F., Halla Bldg., 641-17,
Yoksam-dong, Kangnam-gu, Seoul 135-080 (KR).

(22) International Filing Date: 16 October 2003 (16.10.2003)

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CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE,
GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR,
KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,
MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT,
RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR,
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60/419,912	18 October 2002 (18.10.2002)	US
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60/438,278	3 January 2003 (03.01.2003)	US

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European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO,
SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM,
GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Published:

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[KR/US]; 8730 Costa Verde Boulevard, Apt #2223, San

(48) Date of publication of this corrected version:

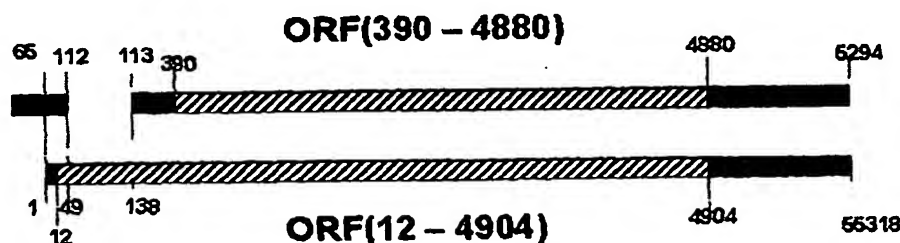
22 July 2004

(15) Information about Correction:

see PCT Gazette No. 30/2004 of 22 July 2004, Section II

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: GENE FAMILIES ASSOCIATED WITH CANCERS



Clone A

Clone B

(57) Abstract: The invention relates generally to the changes in gene expression in human tissues from cancer patients. The invention relates specifically to human gene families which are differentially expressed in cancer tissues of breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach compared to corresponding normal tissues.

WO 2004/035789 A1

GENE FAMILIES ASSOCIATED WITH CANCERS

FIELD OF THE INVENTION

5 The present invention relates to the changes in gene expression in human tissues from cancer patients. The invention specifically relates to human genes which are differentially expressed in cancer tissues of breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach compared to corresponding normal tissues.

BACKGROUND OF THE INVENTION

10 In the United States, more than one million new cancer cases are diagnosed and about half million people die of cancer. The causes of cancer are many and varied, and include genetic predisposition, environmental influences, infectious agents and ageing. These transform normal cells into cancerous ones by derailing a wide spectrum of regulatory and downstream effector pathways. Several essential alterations in cell
15 physiology collectively dictate malignant growth: self-sufficiency in growth signals, insensitivity to growth-inhibitory signals, evasion of programmed cell death, limitless replicative potential, sustained angiogenesis, and tissue invasion and metastasis (Hanahan and Weinberg (2000), *Cell* 100:57-70).

To date, researchers have been able to identify many genetic alterations believed to
20 underlie tumor development. These genetic alterations include amplification of oncogenes and mutations that result in the loss of tumor suppressor genes. Oncogenes were initially identified as genes carried by viruses that cause transformation of their target cells. A major class of the viral oncogenes have cellular counterparts that are involved in normal cell functions. The cellular genes are called proto-oncogene, and in certain cases their
25 mutation or aberrant in the cell is associated with tumor formation. The generation of a

oncogene represents a gain-of-function in which a cellular proto-oncogene is inappropriately activated. This can involve a mutational change in the protein, or constitutive activation, over-expression, or failure to turn off expression at the appropriate time. About 100 oncogenes have been identified. Examples of oncogenes include, but are not limited to, ras, fos, myc, abl, and myb (Ponder (2001), *Nature* 411:336-341). Tumor suppressor genes, in their wild-type alleles, express proteins that suppress abnormal cellular proliferation. When the gene coding for a tumor suppressor protein is mutated or deleted, the resulting mutant protein or the complete lack of tumor suppressor protein expression may fail to correctly regulate cellular proliferation, and abnormal proliferation may take place, particularly if there is already existing damage to the cellular regulatory mechanism. A number of well-studied human tumors and tumor cell lines have missing or non-functional tumor suppressor genes. Examples of tumor suppressor genes include, but are not limited to, the retinoblastoma susceptibility gene or RB gene, the p53 gene, the deletion in colon carcinoma (DCC) gene and the neurofibromatosis type 1 (NF-1) tumor suppressor gene (Weinberg (1991), *Science* 254:1138-1146). Loss-of-function or inactivation of tumor suppressor genes may play a central role in the initiation and/or progression of a significant number of human cancers.

The utilization of genome-wide expression profiles to classify tumors, to identify drug targets, to identify diagnostic markers and/or to gain further insights into the consequences of chemotherapeutic treatments could facilitate the design of more efficacious stratagems for treating a variety of cancers. Initial studies utilizing gene expression patterns to identify subtypes of cancer produced rather intriguing results (see Perou *et al.* (1999), *Proc Natl Acad Sci U S A* 96:9212-9217; Golub *et al.* (1999), *Science* 286:531-537; Alizadeh *et al.* (2000), *Nature* 403:503-511; Alon *et al.* (1999), *Proc Natl Acad Sci U S A* 96:6745-6750; and Bittner *et al.* (2000), *Nature* 406:536-540; Perou *et al.* (2000), *Nature* 406:747-752). Molecular classification of B-cell lymphoma by gene expression profiling elucidated clinically distinct diffuse large-B-cell lymphoma subgroups (see Alizadeh *et al.*, supra). In breast cancer, studies utilizing limited numbers

of genes (8,102 genes) have classified tumors into subtypes based on gene expression profiles, and this study indicated a diversity of molecular phenotypes associated with breast tumors (see Perou *et al.*, supra). In addition, the expression profiling has enabled researchers to map tissue-specific expression levels for thousands of genes (Alon *et al.*
5 (1999), *Proc Natl Acad Sci USA* 96:6745-6750; Iyer *et al.* (1999), *Science* 283:83-87; Khan *et al.* (1998), *Cancer Res* 58:5009-5013; Lee *et al.* (1999), *Science* 285:1390-1393; Wang *et al.* (1999), *Gene* 229:101-108; Whitney *et al.* (1999), *Ann Neurol* 46:425-428). Although these studies have demonstrated that expression profiling may be used to produce improvements in diagnosis of human diseases such as cancer, as well as in the
10 development of improved therapeutic strategies, further studies are needed.

Although cancers are diverse and heterogeneous as they are derived from numerous tissues and multiple etiologic factors, it has been suggested that underlying this variability lies a relatively small number of critical events whose convergence is required for the development of any and all cancers (Evan and Vousden (2001), *Nature* 411:342-
15 348). Accordingly, there exists a need for the comprehensive investigation of the changes in global gene expression levels in many different types of cancers to identify critical molecular markers associated with the development and progression of cancer. There remains a need in the art for materials and methods that permit a more accurate diagnosis of cancer. In addition, there remains a need in the art for methods to treat and methods to
20 identify agents that can effectively treat this disease. The present invention meets these and other needs.

SUMMARY OF THE INVENTION

The present invention is based on new genes that are differentially expressed in cancer tissues compared to normal tissues, hereinafter LFG1, LFG2, LFG3, LFG4, LFG5,
25 LFG6, respectively. The invention includes isolated nucleic acid molecules comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 or the complement thereof.

The present invention further includes the nucleic acid molecules operably linked to one or more expression control elements, including vectors comprising the isolated nucleic acid molecules. The invention further includes host cells transformed to contain the nucleic acid molecules of the invention and methods for producing a protein
5 comprising the step of culturing a host cell transformed with a nucleic acid molecule of the invention under conditions in which the protein is expressed.

The invention further provides an isolated polypeptide selected from the group consisting of an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising a fragment of at least 10
10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and an isolated polypeptide comprising naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Polypeptides of the invention also include polypeptides with an amino acid sequence having at least about 50%, 60%, 70%
15 or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

The present invention further provides methods of identifying other members of
20 the polypeptide family of the invention. Specifically, the nucleic acid sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 can be used as a probe, or to generate PCR primers, in methods to identify nucleic acid molecules that encode other members of the LFG1, LFG2, LFG3, LFG4, LFG5 or LFG6 family of proteins.

The invention further provides an isolated antibody or antigen-binding antibody
25 fragment that specifically binds to a polypeptide of the invention, including monoclonal and polyclonal antibodies.

The invention further provides methods of identifying an agent which modulates the expression of a nucleic acid molecule encoding a protein of the invention, comprising: exposing cells which express the nucleic acid molecule to the agent; and determining whether the agent modulates expression of said nucleic acid molecule, thereby identifying
5 an agent which modulates the expression of a nucleic acid molecule encoding the protein.

The invention further provides methods of identifying an agent which modulates the level of or at least one activity of a protein of the invention, comprising: exposing cells which express the protein to the agent; and determining whether the agent modulates the level of or at least one activity of said protein, thereby identifying an agent which
10 modulates the level of or at least one activity of the protein.

The present invention further provides methods of modulating the expression of a nucleic acid molecule encoding a protein of the invention, comprising the step of administering an effective amount of an agent which modulates the expression of a nucleic acid molecule encoding the protein. The invention also provides methods of modulating
15 at least one activity of a protein of the invention, comprising the step of administering an effective amount of an agent which modulates at least one activity of the protein of the invention.

The invention further provides methods of identifying binding partners for a protein of the invention, comprising the steps of exposing said protein to a potential
20 binding partner; and determining if the potential binding partner binds to said protein, thereby identifying binding partners for the protein.

The present invention further provides methods to identify agents that can block or modulate the association of a protein of the invention with a binding partner. Specifically, an agent can be tested for the ability to block, reduce or otherwise modulate the
25 association of a protein of invention with a binding partner by contacting said protein, or a fragment thereof, and a binding partner with a test agent and determining whether the test agent blocks or reduces the binding of the protein of invention to the binding partner.

The present invention further provides methods for reducing or blocking the association of a protein of invention with one or more of its binding partners, comprising the step of administering an effective amount of an agent which reduces or blocks the binding of said protein to the binding partner. The method can utilize an agent that binds
5 to the protein of invention or to the binding partner.

In accordance with another aspect of the invention, the proteins of the invention can be used as starting points for rational drug design to provide ligands, therapeutic drugs or other types of small chemical molecules. Alternatively, small molecules or other compounds identified by the above-described screening assays may serve as “lead
10 compounds” in rational drug design.

The present invention further relates to a process for treating cancer comprising inserting into a cancerous cell a nucleic acid construct comprising the nucleic acid molecules of the invention operably linked to a promoter or enhancer element such that expression of said nucleic acid molecule causes suppression of said cancer.

15 The present invention further includes non-human transgenic animals modified to contain the nucleic acid molecules of the invention, or non-human transgenic animals modified to contain the mutated nucleic acid molecules such that expression of the encoded polypeptides of the invention is prevented.

The present invention also includes non-human transgenic animals in which all or
20 a portion of a gene comprising all or a portion of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 has been knocked out or deleted from the genome of the animal.

The invention further provides methods of diagnosing cancers, comprising the steps of acquiring a tissue, blood, urine or other sample from a subject and determining the level of expression of a nucleic acid molecule of the invention or polypeptide of the
25 invention.

The invention further includes compositions comprising a diluent and a polypeptide or protein selected from the group consisting of an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising a fragment of at least 10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and an isolated polypeptide with an amino acid sequence having at least about 50%, 60%, 70% or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the relative alignment positions of the two LFG1 clones.

Figure 2 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG1-Clone A (SEQ ID NO: 2). Analysis was performed according to the method of Kyte-Doolittle.

Figure 3 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG1-Clone B (SEQ ID NO: 4). Analysis was performed according to the method of Kyte-Doolittle.

Figure 4 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG2 (SEQ ID NO: 6). Analysis was performed according to the method of Kyte-Doolittle.

Figure 5 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG3 (SEQ ID NO: 8). Analysis was performed according to the method of Kyte-Doolittle.

Figure 6 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG4 (SEQ ID NO: 10). Analysis was performed according to the method of Kyte-Doolittle.

Figure 7 is a hydrophobicity plot of the protein encoded by the open reading frame of ALFG5 (SEQ ID NO: 12). Analysis was performed according to the method of Kyte-Doolittle.

Figure 8 shows the relative alignment positions of the two LFG6 clones.

Figure 9 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG6-#20 (SEQ ID NO: 14). Analysis was performed according to the method of Kyte-Doolittle.

Figure 10 is a hydrophobicity plot of the protein encoded by the open reading frame of LFG6-#46 (SEQ ID NO: 16). Analysis was performed according to the method of Kyte-Doolittle.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

I. General Description

The present invention is based in part on the identification of new gene families that are differentially expressed in cancerous human tissues compared to normal human tissues. These gene families correspond to the human cDNA of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 and 15.

The genes and proteins of the invention may be used as diagnostic agents or markers to detect cancer or to differentiate carcinoma from normal tissue in a sample. They can also serve as a target for agents that modulate gene expression or activity. For example, agents may be identified that modulate biological processes associated with tumor growth, including the hyperplastic process of cancer.

II. Specific Embodiments

A. The Proteins Associated with Cancer

The present invention provides isolated proteins, allelic variants of the proteins, and conservative amino acid substitutions of the proteins. As used herein, the “protein” or “polypeptide” refers, in part, to a protein that has the human amino acid sequence depicted in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. The terms also refer to naturally occurring allelic variants and proteins that have a slightly different amino acid sequence than that specifically recited above. Allelic variants, though possessing a slightly different amino acid sequence than those recited above, will still have the same or similar biological functions associated with these proteins.

As used herein, the family of proteins related to the human amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 refers to proteins that have been isolated from organisms in addition to humans. The methods used to identify and isolate other members of the family of proteins related to these proteins are described below.

The proteins of the present invention are preferably in isolated form. As used herein, a protein is said to be isolated when physical, mechanical or chemical methods are employed to remove the protein from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated protein.

The proteins of the present invention further include insertion, deletion or conservative amino acid substitution variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. As used herein, a conservative variant refers to alterations in the amino acid sequence that do not adversely affect the biological functions of the protein. A substitution, insertion or deletion is said to adversely affect the protein when the altered sequence prevents or disrupts a biological function associated with the protein. For example, the overall charge, structure or hydrophobic/hydrophilic properties of the protein, in certain instances, may be altered without adversely affecting a biological activity. Accordingly, the amino acid sequence can be altered, for example to render the peptide more hydrophobic or hydrophilic, without adversely affecting the biological activities of the protein.

Ordinarily, the allelic variants, the conservative substitution variants, and the members of the protein family, will have an amino acid sequence having at least about 50%, 60%, 70% or 75% amino acid sequence identity with the sequence set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, more preferably at least about 80%, even more preferably at least about 90-95%, and most preferably at least about 95-98% sequence identity. Identity or homology with respect to such sequences is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent homology, and not considering any conservative substitutions as part of the sequence identity (see section B for the relevant parameters). Fusion proteins, or N-terminal, C-terminal or internal extensions, deletions, or insertions into the peptide sequence shall not be construed as affecting homology.

Thus, the proteins of the present invention include molecules having the amino acid sequence disclosed in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; fragments thereof having a consecutive sequence of at least about 3, 4, 5, 6, 10, 15, 20, 25, 30, 35 or more amino acid residues of these proteins; amino acid sequence variants wherein one or more amino acid residues has been inserted N- or C-terminal to, or within, the disclosed coding sequence; and amino acid sequence variants of the disclosed sequence, or their fragments

as defined above, that have been substituted by at least one residue. Such fragments, also referred to as peptides or polypeptides, may contain antigenic regions, functional regions of the protein identified as regions of the amino acid sequence which correspond to known protein domains, as well as regions of pronounced hydrophilicity. The regions are all easily identifiable by using commonly available protein sequence analysis software such as MacVector (Oxford Molecular).

Contemplated variants further include those containing predetermined mutations by, *e.g.*, homologous recombination, site-directed or PCR mutagenesis, and the corresponding proteins of other animal species, including but not limited to rabbit, mouse, rat, porcine, bovine, ovine, equine and non-human primate species, and the alleles or other naturally occurring variants of the family of proteins; and derivatives wherein the protein has been covalently modified by substitution, chemical, enzymatic, or other appropriate means with a moiety other than a naturally occurring amino acid (for example a detectable moiety such as an enzyme or radioisotope).

The present invention further provides compositions comprising a protein or polypeptide of the invention and a diluent. Suitable diluents can be aqueous or non-aqueous solvents or a combination thereof, and can comprise additional components, for example water-soluble salts or glycerol, that contribute to the stability, solubility, activity, and/or storage of the protein or polypeptide.

As described below, members of the families of proteins can be used: (1) to identify agents which modulate the level of or at least one activity of the protein, (2) to identify binding partners for the protein, (3) as an antigen to raise polyclonal or monoclonal antibodies, (4) as a therapeutic agent or target and (5) as a diagnostic agent or marker of cancer.

B. Nucleic Acid Molecules

The present invention further provides nucleic acid molecules that encode the protein having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 and the related proteins herein described, preferably in isolated form. As used herein, "nucleic acid" is defined as RNA or DNA that encodes a protein or peptide as defined above, is complementary to a nucleic acid sequence encoding such peptides, hybridizes to the nucleic acid of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 and remains stably bound to it under appropriate stringency conditions, encodes a polypeptide sharing at least about 50%, 60%, 70% or 75%, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% or more identity with the peptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 or exhibits at least 50%, 60%, 70% or 75%, preferably at least about 80%, more preferably at least about 90-95%, and most preferably at least about 95-98% or more nucleotide sequence identity over the open reading frames of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15.

The present invention further includes isolated nucleic acid molecules that specifically hybridize to the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, particularly molecules that specifically hybridize over the open reading frames. Such molecules that specifically hybridize to the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 typically do so under stringent hybridization conditions.

Specifically contemplated are genomic DNA, cDNA, mRNA and antisense molecules, as well as nucleic acids based on alternative backbones or including alternative bases, whether derived from natural sources or synthesized. Such hybridizing or complementary nucleic acids, however, are defined further as being novel and unobvious over any prior art nucleic acid including that which encodes, hybridizes under appropriate stringency conditions, or is complementary to nucleic acid encoding a protein according to the present invention.

Homology or identity at the nucleotide or amino acid sequence level is determined by BLAST (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs blastp, blastn, blastx, tblastn and tblastx (Altschul *et al.* (1997), *Nucleic*

Acids Res. 25: 3389-3402, and Karlin *et al.* (1990), *Proc. Natl. Acad. Sci. USA* 87: 2264-2268, both fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the BLAST program is to first consider similar segments, with and without gaps, between a query sequence and a database sequence, then to
5 evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.* (1994), *Nat. Genet.* 6: 119-129 which is fully incorporated by reference. The search parameters for histogram, descriptions, alignments, expect (*i.e.*, the statistical significance
10 threshold for reporting matches against database sequences), cutoff, matrix and filter (low complexity) are at the default settings. The default scoring matrix used by blastp, blastx, tblastn, and tblastx is the BLOSUM62 matrix (Henikoff *et al.* (1992), *Proc. Natl. Acad. Sci. USA* 89: 10915-10919, fully incorporated by reference), recommended for query sequences over 85 nucleotides or amino acids in length.

15 For blastn, the scoring matrix is set by the ratios of M (*i.e.*, the reward score for a pair of matching residues) to N (*i.e.*, the penalty score for mismatching residues), wherein the default values for M and N are 5 and -4, respectively. Four blastn parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the
20 window width within which gapped alignments are generated). The equivalent Blastp parameter settings were Q=9; R=2; wink=1; and gapw=32. A Bestfit comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

25 “Stringent conditions” are those that (1) employ low ionic strength and high temperature for washing, for example, 0.015 M NaCl/0.0015 M sodium citrate/0.1% SDS at 50°C, or (2) employ during hybridization a denaturing agent such as formamide, for

example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM NaCl, 75 mM sodium citrate at 42°C. Another example is hybridization in 50% formamide, 5× SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2× SSC and 0.1% SDS. A skilled artisan can readily determine and vary the stringency conditions appropriately to obtain a clear and detectable hybridization signal. Preferred molecules are those that hybridize under the above conditions to the complement of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 and which encode a functional or full-length protein. Even more preferred hybridizing molecules are those that hybridize under the above conditions to the complement strand of the open reading frame of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15.

As used herein, a nucleic acid molecule is said to be "isolated" when the nucleic acid molecule is substantially separated from contaminant nucleic acid molecules encoding other polypeptides.

The present invention further provides fragments of the disclosed nucleic acid molecules. As used herein, a fragment of a nucleic acid molecule refers to a small portion of the coding or non-coding sequence. The size of the fragment will be determined by the intended use. For example, if the fragment is chosen so as to encode an active portion of the protein, the fragment will need to be large enough to encode the functional region(s) of the protein. For instance, fragments which encode peptides corresponding to predicted antigenic regions may be prepared. If the fragment is to be used as a nucleic acid probe or PCR primer, then the fragment length is chosen so as to obtain a relatively small number of false positives during probing/priming (see the discussion in Section G).

Fragments of the nucleic acid molecules of the present invention (*i.e.*, synthetic oligonucleotides) that are used as probes or specific primers for the polymerase chain reaction (PCR), or to synthesize gene sequences encoding proteins of the invention, can

easily be synthesized by chemical techniques, for example, the phosphoramidite method of Matteucci *et al.*, ((1981) *J. Am. Chem. Soc.* 103: 3185-3191) or using automated synthesis methods. In addition, larger DNA segments can readily be prepared by well known methods, such as synthesis of a group of oligonucleotides that define various modular segments of the gene, followed by ligation of oligonucleotides to build the complete modified gene.

The nucleic acid molecules of the present invention may further be modified so as to contain a detectable label for diagnostic and probe purposes. A variety of such labels are known in the art and can readily be employed with the encoding molecules herein described. Suitable labels include, but are not limited to, biotin, radiolabeled or fluorescently labeled nucleotides and the like. A skilled artisan can readily employ any such label to obtain labeled variants of the nucleic acid molecules of the invention.

C. Isolation of Other Related Nucleic Acid Molecules

As described above, the identification and characterization of the nucleic acid molecule having SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 allows a skilled artisan to isolate nucleic acid molecules that encode other members of the protein family in addition to the sequences herein described. Further, the presently disclosed nucleic acid molecules allow a skilled artisan to isolate nucleic acid molecules that encode other members of the family of proteins in addition to the proteins having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

For instance, a skilled artisan can readily use the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 to generate antibody probes to screen expression libraries prepared from appropriate cells. Typically, polyclonal antiserum from mammals such as rabbits immunized with the purified protein (as described below) or monoclonal antibodies can be used to probe a mammalian cDNA or genomic expression library, such as lambda gtlI library, to obtain the appropriate coding sequence for other members of the protein family. The cloned cDNA sequence can be expressed as a fusion protein,

expressed directly using its own control sequences, or expressed by constructions using control sequences appropriate to the particular host used for expression of the enzyme.

Alternatively, a portion of the coding sequence herein described can be synthesized and used as a probe to retrieve DNA encoding a member of the protein family from any mammalian organism. Oligomers containing approximately 18-20 nucleotides (encoding about a 6-7 amino acid stretch) are prepared and used to screen genomic DNA or cDNA libraries to obtain hybridization under stringent conditions or conditions of sufficient stringency to eliminate an undue level of false positives.

Additionally, pairs of oligonucleotide primers can be prepared for use in PCR to selectively clone an encoding nucleic acid molecule. A PCR denature/anneal/extend cycle for using such PCR primers is well known in the art and can readily be adapted for use in isolating other encoding nucleic acid molecules.

Nucleic acid molecules encoding other members of the protein family may also be identified in existing genomic or other sequence information using any available computational method, including but not limited to: PSI-BLAST (Altschul *et al.* (1997), *Nucl. Acids Res.* 25: 3389-3402); PHI-BLAST (Zhang *et al.* (1998), *Nucl. Acids Res.* 26: 3986-3990), 3D-PSSM (Kelly *et al.* (2000), *J. Mol. Biol.* 299: 499-520); and other computational analysis methods (Shi *et al.* (1999), *Biochem. Biophys. Res. Commun.* 262: 132-138 and Matsunami *et al.* (2000), *Nature* 404: 601-604).

D. rDNA molecules Containing a Nucleic Acid Molecule

The present invention further provides recombinant DNA molecules (rDNAs) that contain a coding sequence. As used herein, a rDNA molecule is a DNA molecule that has been subjected to molecular manipulation *in situ*. Methods for generating rDNA molecules are well known in the art, for example, see Sambrook *et al.*, Molecular Cloning- A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold

Spring Harbor, NY, 2001. In the preferred rDNA molecules, a coding DNA sequence is operably linked to expression control sequences and/or vector sequences.

5 The choice of vector and/or expression control sequences to which one of the protein family encoding sequences of the present invention is operably linked depends directly, as is well known in the art, on the functional properties desired, *e.g.*, protein expression, and the host cell to be transformed. A vector contemplated by the present invention is at least capable of directing the replication or insertion into the host chromosome, and preferably also expression, of the structural gene included in the rDNA molecule.

10 Expression control elements that are used for regulating the expression of an operably linked protein encoding sequence are known in the art and include, but are not limited to, inducible promoters, constitutive promoters, secretion signals, and other regulatory elements. Preferably, the inducible promoter is readily controlled, such as being responsive to a nutrient in the host cell's medium.

15 In one embodiment, the vector containing a coding nucleic acid molecule will include a prokaryotic replicon, *i.e.*, a DNA sequence having the ability to direct autonomous replication and maintenance of the recombinant DNA molecule extrachromosomally in a prokaryotic host cell, such as a bacterial host cell, transformed therewith. Such replicons are well known in the art. In addition, vectors that include a
20 prokaryotic replicon may also include a gene whose expression confers a detectable marker such as a drug resistance. Typical bacterial drug resistance genes are those that confer resistance to ampicillin, kanamycin, chloramphenicol or tetracycline.

Vectors that include a prokaryotic replicon can further include a prokaryotic or bacteriophage promoter capable of directing the expression (transcription and translation)
25 of the coding gene sequences in a bacterial host cell, such as *E. coli*. A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with bacterial

hosts are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention. Typical of such vector plasmids are pUC8, pUC9, pBR322 and pBR329 available from BioRad Laboratories, (Richmond, CA), pPL and pKK223 available from Pharmacia (Piscataway, NJ).

5 Expression vectors compatible with eukaryotic cells, preferably those compatible with vertebrate cells, can also be used to form rDNA molecules that contain a coding sequence. Eukaryotic cell expression vectors, including viral vectors, are well known in the art and are available from several commercial sources. Typically, such vectors are provided containing convenient restriction sites for insertion of the desired DNA segment.

10 Typical of such vectors are pSVL and pKSV-10 (Pharmacia), pBPV-1/pML2d (International Biotechnologies, Inc.), pTDT1 (ATCC, #31255), the vector pCDM8 described herein, and the like eukaryotic expression vectors. Vectors may be modified to include tissue specific promoters if needed.

Eukaryotic cell expression vectors used to construct the rDNA molecules of the present invention may further include a selectable marker that is effective in an eukaryotic cell, preferably a drug resistance selection marker. A preferred drug resistance marker is the gene whose expression results in neomycin resistance, *i.e.*, the neomycin phosphotransferase (*neo*) gene. (Southern *et al.* (1982), *J. Mol. Anal. Genet.* 1:327-341). Alternatively, the selectable marker can be present on a separate plasmid, and the two

15 vectors are introduced by co-transfection of the host cell, and selected by culturing in the appropriate drug for the selectable marker.

20

E. Host Cells Containing an Exogenously Supplied Coding Nucleic Acid Molecule

The present invention further provides host cells transformed with a nucleic acid molecule that encodes a protein of the present invention. The host cell can be either

25 prokaryotic or eukaryotic. Eukaryotic cells useful for expression of a protein of the invention are not limited, so long as the cell line is compatible with cell culture methods

and compatible with the propagation of the expression vector and expression of the gene product. Preferred eukaryotic host cells include, but are not limited to, yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human cell line. Preferred eukaryotic host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells (NIH/3T3) available from the ATCC as CRL 1658, baby hamster kidney cells (BHK), and the like eukaryotic tissue culture cell lines.

Any prokaryotic host can be used to express a rDNA molecule encoding a protein of the invention. The preferred prokaryotic host is *E. coli*.

Transformation of appropriate cell hosts with a rDNA molecule of the present invention is accomplished by well known methods that typically depend on the type of vector used and host system employed. With regard to transformation of prokaryotic host cells, electroporation and salt treatment methods are typically employed (see, for example, Cohen *et al.* (1972), *Proc. Natl. Acad. Sci. USA* 69: 2110; and Sambrook *et al.*, *supra*). With regard to transformation of vertebrate cells with vectors containing rDNAs, electroporation, cationic lipid or salt treatment methods are typically employed, see, for example, Graham *et al.* (1973), *Viol.* 52: 456; Wigler *et al.* (1979), *Proc. Natl. Acad. Sci. USA* 76: 1373-1376.

Successfully transformed cells, *i.e.*, cells that contain a rDNA molecule of the present invention, can be identified by well known techniques including the selection for a selectable marker. For example, cells resulting from the introduction of an rDNA of the present invention can be cloned to produce single colonies. Cells from those colonies can be harvested, lysed and their DNA content examined for the presence of the rDNA using a method such as that described by Southern, (1975) *J. Mol. Biol.* 98: 503 or Berent *et al.*, (1985) *Biotech.* 3: 208, or the proteins produced from the cell assayed via an immunological method.

F. Production of Recombinant Proteins using a rDNA Molecule

The present invention further provides methods for producing a protein of the invention using nucleic acid molecules herein described. In general terms, the production of a recombinant form of a protein typically involves the following steps:

5 First, a nucleic acid molecule is obtained that encodes a protein of the invention, such as a nucleic acid molecule comprising, consisting essentially of or consisting of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, or nucleotides 390-4883 or 390-4880 of SEQ ID NO: 1, or nucleotides 12-4907 or 12-4904 of SEQ ID NO: 3, or nucleotides 424-1911 or 424-1908 of SEQ ID NO: 5, or nucleotides 405-1838 or 405-1835 of SEQ ID NO: 7, or
10 nucleotides 89-1153 or 89-1150 of SEQ ID NO: 9, or nucleotides 223-1572 or 223-1569 of SEQ ID NO: 11, or 418-1395 or 418-1392 of SEQ ID NO: 13, or nucleotides 271-1434 or 271-1431 of SEQ ID NO: 15. If the encoding sequence is uninterrupted by introns, as are these open-reading-frames, it is directly suitable for expression in any host.

The nucleic acid molecule is then preferably placed in operable linkage with
15 suitable control sequences, as described above, to form an expression unit containing the protein open reading frame. The expression unit is used to transform a suitable host and the transformed host is cultured under conditions that allow the production of the recombinant protein. Optionally the recombinant protein is isolated from the medium or from the cells; recovery and purification of the protein may not be necessary in some
20 instances where some impurities may be tolerated.

Each of the foregoing steps can be done in a variety of ways. For example, the desired coding sequences may be obtained from genomic fragments and used directly in appropriate hosts. The construction of expression vectors that are operable in a variety of
25 hosts is accomplished using appropriate replicons and control sequences, as set forth above. The control sequences, expression vectors, and transformation methods are dependent on the type of host cell used to express the gene and were discussed in detail earlier. Suitable restriction sites can, if not normally available, be added to the ends of the

coding sequence so as to provide an excisable gene to insert into these vectors. A skilled artisan can readily adapt any host/expression system known in the art for use with the nucleic acid molecules of the invention to produce recombinant protein.

G. Methods to Identify Agents that Modulate the Expression of a Nucleic Acid
5 Encoding the Genes Associated with Cancer

Another embodiment of the present invention provides methods for identifying agents that modulate the expression of a nucleic acid encoding a protein of the invention such as a protein having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Such assays may utilize any available means of monitoring for changes in the
10 expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell.

In one assay format, cell lines that contain reporter gene fusions between nucleotides from within the open reading frame defined by nucleotides 390-4883 of SEQ
15 ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1911 of SEQ ID NO: 5, nucleotides 405-1838 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1572 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, nucleotides 271-1434 of SEQ ID NO: 15, and/or the 5' and/or 3' regulatory elements and any assayable fusion partner may be prepared. Numerous assayable fusion partners are
20 known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.* (1990), *Anal. Biochem.* 188: 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which
25 modulate the expression of a nucleic acid of the invention.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a nucleic acid encoding a protein of the invention, such as the protein having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. For instance, mRNA expression may be monitored directly by hybridization to the nucleic acids of the invention. Cell lines are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, Molecular Cloning - A Laboratory Manual, Third Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001.

The preferred cells will be those derived from human tissue, for instance, biopsy tissue or cultured cells from patients with cancer. Cell lines such as ATCC breast ductal carcinoma cell lines (Catalogue Nos. CRL-2320, CRL-2338, and CRL-7345), ATCC colorectal adenocarcinoma cell lines (Catalogue Nos. CCL-222, CCL-224, CCL-225, CCL-234, CRL-7159, and CRL-7184), ATCC kidney clear cell carcinoma cell lines (Catalogue Nos. HTB-46 and HTB-47), ATCC renal cell adenocarcinoma cell lines (Catalogue Nos. CRL-1611, CRL-1932 and CRL-1933), ATCC liver hepatocellular carcinoma cell lines (Catalogue Nos. CRL-2233, CRL-2234, and HB-8065), ATCC lung adenocarcinoma cell lines (Catalogue Nos. CRL-5944, CRL-7380, and CRL-5907), ATCC lymphoma cell lines (Catalogue Nos. CRL-7936, CRL-7264, and CRL-7507), ATCC ovary adenocarcinoma cell lines (Catalogue Nos. HTB-161, HTB-75, and HTB-76), ATCC pancreas adenocarcinoma cell lines (Catalogue Nos. CRL-1687, CRL-2119, and HTP-79), prostate adenocarcinoma cell lines (Catalogue Nos. CRL-1435, CRL-2422, and CRL-2220), and ATCC gastric adenocarcinoma cell lines (Catalogue Nos. CRL-1739, CRL-1863, and CRL-1864) may be used. Alternatively, other available cells or cell lines may be used.

Probes to detect differences in RNA expression levels between cells exposed to the agent and control cells may be prepared from the nucleic acids of the invention. It is preferable, but not necessary, to design probes which hybridize only with target nucleic acids under conditions of high stringency. Only highly complementary nucleic acid

hybrids form under conditions of high stringency. Accordingly, the stringency of the assay conditions determines the amount of complementarity which should exist between two nucleic acid strands in order to form a hybrid. Stringency should be chosen to maximize the difference in stability between the probe:target hybrid and probe:non-target hybrids.

Probes may be designed from the nucleic acids of the invention through methods known in the art. For instance, the G+C content of the probe and the probe length can affect probe binding to its target sequence. Methods to optimize probe specificity are commonly available in Sambrook *et al.*, *supra*, or Ausubel *et al.*, Short Protocols in Molecular Biology, Fourth Ed., John Wiley & Sons, Inc., New York, 1999.

Hybridization conditions are modified using known methods, such as those described by Sambrook *et al.* and Ausubel *et al.* as required for each probe. Hybridization of total cellular RNA or RNA enriched for polyA RNA can be accomplished in any available format. For instance, total cellular RNA or RNA enriched for polyA RNA can be affixed to a solid support and the solid support exposed to at least one probe comprising at least one, or part of one of the sequences of the invention under conditions in which the probe will specifically hybridize. Alternatively, nucleic acid fragments comprising at least one, or part of one of the sequences of the invention can be affixed to a solid support, such as a silicon chip, porous glass wafer or membrane. The solid support can then be exposed to total cellular RNA or polyA RNA from a sample under conditions in which the affixed sequences will specifically hybridize. Such solid supports and hybridization methods are widely available, for example, those disclosed by Beattie, (1995) WO 95/11755. By examining for the ability of a given probe to specifically hybridize to an RNA sample from an untreated cell population and from a cell population exposed to the agent, agents which up- or down-regulate the expression of a nucleic acid encoding the protein having the sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 are identified.

Hybridization for qualitative and quantitative analysis of mRNAs may also be carried out by using a RNase Protection Assay (*i.e.*, RPA, see Ma *et al.* (1996), *Methods* 10: 273-238). Briefly, an expression vehicle comprising cDNA encoding the gene product and a phage specific DNA dependent RNA polymerase promoter (*e.g.*, T7, T3 or SP6 RNA polymerase) is linearized at the 3' end of the cDNA molecule, downstream from the phage promoter, wherein such a linearized molecule is subsequently used as a template for synthesis of a labeled antisense transcript of the cDNA by *in vitro* transcription. The labeled transcript is then hybridized to a mixture of isolated RNA (*i.e.*, total or fractionated mRNA) by incubation at 45°C overnight in a buffer comprising 80% formamide, 40 mM Pipes, pH 6.4, 0.4 M NaCl and 1 mM EDTA. The resulting hybrids are then digested in a buffer comprising 40 µg/ml ribonuclease A and 2 µg/ml ribonuclease. After deactivation and extraction of extraneous proteins, the samples are loaded onto urea/polyacrylamide gels for analysis.

In another assay, to identify agents which affect the expression of the instant gene products, cells or cell lines are first identified which express the gene products of the invention physiologically. Cells and/or cell lines so identified would be expected to comprise the necessary cellular machinery such that the fidelity of modulation of the transcriptional apparatus is maintained with regard to exogenous contact of agent with appropriate surface transduction mechanisms and/or the cytosolic cascades. Further, such cells or cell lines would be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) construct comprising an operable non-translated 5' promoter-containing end of the structural gene encoding the instant gene products fused to one or more antigenic fragments, which are peculiar to the instant gene products, wherein said fragments are under the transcriptional control of said promoter and are expressed as polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides or may further comprise an immunologically distinct tag or other detectable marker. Such a process is well known in the art (see Sambrook *et al.*, *supra*).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions. For example, the agent in a pharmaceutically acceptable excipient is contacted with cells in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and/or serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the “agent-contacted” sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the “agent-contacted” sample compared to the control will be used to distinguish the effectiveness of the agent.

15 H. Methods to Identify Agents that Modulate the Level or at Least One Activity of the Cancer Associated Proteins

Another embodiment of the present invention provides methods for identifying agents that modulate the level or at least one activity of a protein of the invention such as the protein having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16. Such methods or assays may utilize any means of monitoring or detecting the desired activity and are particularly useful for identifying agents that treat cancer.

In one format, the relative amounts of a protein of the invention between a cell population that has been exposed to the agent to be tested compared to an un-exposed control cell population may be assayed. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell

line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe.

Antibody probes are prepared by immunizing suitable mammalian hosts in appropriate immunization protocols using the peptides, polypeptides or proteins of the invention if they are of sufficient length, or, if desired, or if required to enhance immunogenicity, conjugated to suitable carriers. Methods for preparing immunogenic conjugates with carriers such as BSA, KLH, or other carrier proteins are well known in the art. In some circumstances, direct conjugation using, for example, carbodiimide reagents may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co. (Rockford, IL), may be desirable to provide accessibility to the hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues, for example, to facilitate linking to a carrier. Administration of the immunogens is conducted generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation.

While the polyclonal antisera produced in this way may be satisfactory for some applications, for pharmaceutical compositions, use of monoclonal preparations is preferred. Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using the standard method of Kohler and Milstein ((1975) *Nature* 256: 495-497) or modifications which effect immortalization of lymphocytes or spleen cells, as is generally known. The immortalized cell lines secreting the desired antibodies are screened by immunoassay in which the antigen is the peptide hapten, polypeptide or protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid.

The desired monoclonal antibodies are then recovered from the culture supernatant or from the ascites supernatant. Fragments of the monoclonal antibodies or the polyclonal

antisera which contain the immunologically significant (antigen-binding) portion can be used as antagonists, as well as the intact antibodies. Use of immunologically reactive (antigen-binding) antibody fragments, such as the Fab, Fab', or F(ab')₂ fragments is often preferable, especially in a therapeutic context, as these fragments are generally less immunogenic than the whole immunoglobulin.

The antibodies or antigen-binding fragments may also be produced, using current technology, by recombinant means. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras with multiple species origin, such as humanized antibodies.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of a protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. Dominant negative proteins, DNAs encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and

functionally similar to the parent peptide (see Grant in: Molecular Biology and Biotechnology, Meyers, ed., pp. 659-664, VCH Publishers, Inc., New York, 1995). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

5 The peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production using solid phase peptide synthesis is necessitated if
10 non-gene-encoded amino acids are to be included.

 Another class of agents of the present invention are antibodies immunoreactive with critical positions of proteins of the invention, e.g., cytoplasmic domain, spacer domain, α -helical coiled-coil domain, or the receptor domain, as described herein. Antibody agents are obtained by immunization of suitable mammalian subjects with
15 peptides, containing as antigenic regions, those portions of the protein intended to be targeted by the antibodies.

I. Uses for Agents that Modulate the Expression or at Least one Activity of the Proteins Associated with Cancer

 As provided in the Examples, the proteins and nucleic acids of the invention, such
20 as the proteins having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, are differentially expressed in cancerous tissue. Agents that up- or down- regulate or modulate the expression of the protein or at least one activity of the protein, such as agonists or antagonists, may be used to modulate biological and pathologic processes associated with the protein's function and activity. This includes agents identified
25 employing homologues and analogues of the present invention.

As used herein, a subject can be any mammal, so long as the mammal is in need of modulation of a pathological or biological process mediated by a protein of the invention. The term "mammal" is defined as an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects.

5 Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression of a protein of the invention may be associated with cell growth or hyperplasia. As used herein, an agent is said to modulate a pathological process when the agent reduces the degree or severity of the process. For instance, cancer may be prevented or disease progression modulated by the administration
10 of agents which up- or down-regulate or modulate in some way the expression or at least one activity of a protein of the invention.

 The agents of the present invention can be provided alone, or in combination with other agents that modulate a particular pathological process. For example, an agent of the present invention can be administered in combination with other known drugs. As used
15 herein, two agents are said to be administered in combination when the two agents are administered simultaneously or are administered independently in a fashion such that the agents will act at the same time.

 The agents of the present invention can be administered via parenteral, subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, or buccal routes.
20 Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

 The present invention further provides compositions containing one or more agents which modulate expression or at least one activity of a protein of the invention. While
25 individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 0.1 to 100 µg/kg body

wt. The preferred dosages comprise 0.1 to 10 $\mu\text{g/kg}$ body wt. The most preferred dosages comprise 0.1 to 1 $\mu\text{g/kg}$ body wt.

In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients
5 and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form, for example, water-soluble salts. In addition, suspensions of the active compounds as appropriate oily injection suspensions may be
10 administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. Optionally, the suspension may also contain stabilizers. Liposomes can also be used to
15 encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic administration of the active ingredient.

20 Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In practicing the methods of this invention, the compounds of this invention may be used alone or in combination, or in combination with other therapeutic or diagnostic
25 agents. In certain preferred embodiments, the compounds of this invention may be coadministered along with other compounds typically prescribed for these conditions according to generally accepted medical practice. The compounds of this invention can be

utilized *in vivo*, ordinarily in mammals, such as humans, sheep, horses, cattle, pigs, dogs, cats, rats and mice, or *in vitro*.

J. Methods to Identify Binding Partners

Another embodiment of the present invention provides methods for isolating and
5 identifying binding partners of proteins of the invention. In general, a protein of the invention is mixed with a potential binding partner or an extract or fraction of a cell under conditions that allow the association of potential binding partners with the protein of the invention. After mixing, peptides, polypeptides, proteins or other molecules that have become associated with a protein of the invention are separated from the mixture. The
10 binding partner that bound to the protein of the invention can then be removed and further analyzed. To identify and isolate a binding partner, the entire protein, for instance a protein comprising the entire amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 can be used. Alternatively, a fragment of the protein can be used.

As used herein, a cellular extract refers to a preparation or fraction which is made
15 from a lysed or disrupted cell. The preferred source of cellular extracts will be cells derived from human tumors or transformed cells, for instance, biopsy tissue or tissue culture cells from carcinomas. Alternatively, cellular extracts may be prepared from normal tissue or available cell lines.

A variety of methods can be used to obtain an extract of a cell. Cells can be
20 disrupted using either physical or chemical disruption methods. Examples of physical disruption methods include, but are not limited to, sonication and mechanical shearing. Examples of chemical lysis methods include, but are not limited to, detergent lysis and enzyme lysis. A skilled artisan can readily adapt methods for preparing cellular extracts in order to obtain extracts for use in the present methods.

25 Once an extract of a cell is prepared, the extract is mixed with the protein of the invention under conditions in which association of the protein with the binding partner can

occur. A variety of conditions can be used, the most preferred being conditions that closely resemble conditions found in the cytoplasm of a human cell. Features such as osmolarity, pH, temperature, and the concentration of cellular extract used, can be varied to optimize the association of the protein with the binding partner.

5 After mixing under appropriate conditions, the bound complex is separated from the mixture. A variety of techniques can be utilized to separate the mixture. For example, antibodies specific to a protein of the invention can be used to immunoprecipitate the binding partner complex. Alternatively, standard chemical separation techniques such as chromatography and density/sediment centrifugation can be used.

10 After removal of non-associated cellular constituents found in the extract, the binding partner can be dissociated from the complex using conventional methods. For example, dissociation can be accomplished by altering the salt concentration or pH of the mixture.

15 To aid in separating associated binding partner pairs from the mixed extract, the protein of the invention can be immobilized on a solid support. For example, the protein can be attached to a nitrocellulose matrix or acrylic beads. Attachment of the protein to a solid support aids in separating peptide/binding partner pairs from other constituents found in the extract. The identified binding partners can be either a single protein or a complex made up of two or more proteins. Alternatively, binding partners may be identified using
20 a Far-Western assay according to the procedures of Takayama *et al.* (1997), *Methods Mol. Biol.* 69: 171-184 or Sauder *et al.* (1996), *J. Gen. Virol.* 77: 991-996 or identified through the use of epitope tagged proteins or GST fusion proteins.

25 Alternatively, the nucleic acid molecules of the invention can be used in a yeast two-hybrid system or other *in vivo* protein-protein detection system. The yeast two-hybrid system has been used to identify other protein partner pairs and can readily be adapted to employ the nucleic acid molecules herein described.

K. Use of the Binding Partners of the Cancer Associated Proteins

Once isolated, the binding partners of the proteins of the invention, and homologues and analogues thereof, obtained using the above described methods can be used for a variety of purposes. The binding partners can be used to generate antibodies
5 that bind to the binding partner using techniques known in the art. Antibodies that bind the binding partner can be used to assay the activity of the protein of the invention, as a therapeutic agent to modulate a biological or pathological process mediated by the protein of the invention, or to purify the binding partner. These uses are described in detail below.

L. Methods to Identify Agents that Block the Associations between the Binding 10 Partners and the Cancer Associated Proteins

Another embodiment of the present invention provides methods for identifying agents that reduce or block the association of a protein of the invention with a binding partner. Specifically, a protein of the invention is mixed with a binding partner in the presence and absence of an agent to be tested. After mixing under conditions that allow
15 association of the proteins, the two mixtures are analyzed and compared to determine if the agent reduced or blocked the association of the protein of the invention with the binding partner. Agents that block or reduce the association of the protein of the invention with the binding partner will be identified as decreasing the amount of association present in the sample containing the tested agent.

20 As used herein, an agent is said to reduce or block the association between a protein of the invention and a binding partner when the presence of the agent decreases the extent to which or prevents the binding partner from becoming associated with the protein of the invention. One class of agents will reduce or block the association by binding to the binding partner while another class of agents will reduce or block the association by
25 binding to the protein of the invention.

The binding partner used in the above assay can either be an isolated and fully characterized protein or can be a partially characterized protein that binds to the protein of the invention or a binding partner that has been identified as being present in a cellular extract. It will be apparent to one of ordinary skill in the art that so long as the binding partner has been characterized by an identifiable property, e.g., molecular weight, the present assay can be used.

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the protein of the invention with the binding partner. An example of randomly selected agents is the use of a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up the contact sites of the binding partner with the protein of the invention. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to the contact site of the protein of the invention on the binding partner. Such an agent will reduce or block the association of the protein of the invention with the binding partner by binding to the binding partner.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates. A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

One class of agents of the present invention are peptide agents whose amino acid sequences are chosen based on the amino acid sequence of the protein of the invention. The peptide agents of the invention can be prepared using standard solid phase (or

solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production using solid phase peptide synthesis is necessitated if
5 non-gene encoded amino acids are to be included.

Another class of agents of the present invention are antibodies immunoreactive with critical positions of the protein of the invention or the binding partner. As described above, antibodies are obtained by immunization of suitable mammalian subjects with peptides, containing as antigenic regions, those portions of the protein of the invention or
10 the binding partner, intended to be targeted by the antibodies. Critical regions include the contact sites involved in the association of the protein of the invention with the binding partner.

As discussed below, the important minimal sequence of residues involved in activity of the protein of the invention define a functional linear domain that can be
15 effectively used as a bait for two hybrid screening and identification of potential associated molecules. Use of such fragments will significantly increase the specificity of the screening as opposed to using the full-length molecule and is therefore preferred. Similarly, this linear sequence can be also used as an affinity matrix also to isolate binding proteins using a biochemical affinity purification strategy.

20 **M. Uses for Agents that Block the Associations between the Binding Partners and the Cancer Associated Proteins**

As provided in the Examples, the proteins and nucleic acids of the invention, such as the proteins having the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, are differentially expressed in cancerous tissue. Agents that reduce or block the
25 interactions of a protein of the invention, including those identified employing

homologues and analogues of the protein, with a binding partner may be used to modulate biological and pathologic processes associated with the protein's function and activity.

As used herein, a subject can be any mammal, so long as the mammal is in need of modulation of a pathological or biological process mediated by a protein of the invention.

5 The term "mammal" is meant an individual belonging to the class Mammalia. The invention is particularly useful in the treatment of human subjects.

Pathological processes refer to a category of biological processes which produce a deleterious effect. For example, expression of a protein of the invention may be associated with cell growth or hyperplasia. As used herein, an agent is said to modulate a

10 pathological process when the agent reduces the degree or severity of the process. For instance, cancer may be prevented or disease progression modulated by the administration of agents that reduce or block the interactions of a protein of the invention with a binding partner.

The agents of the present invention can be administered via parenteral,

15 subcutaneous, intravenous, intramuscular, intraperitoneal, transdermal, or buccal routes. Alternatively, or concurrently, administration may be by the oral route. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

The present invention further provides compositions containing one or more agents

20 that block association of a protein of the invention with a binding partner. While individual needs vary, determination of optimal ranges of effective amounts of each component is within the skill of the art. Typical dosages comprise 0.1 to 100 µg/kg body wt. The preferred dosages comprise 0.1 to 10 µg/kg body wt. The most preferred dosages comprise 0.1 to 1 µg/kg body wt.

25 In addition to the pharmacologically active agent, the compositions of the present invention may contain suitable pharmaceutically acceptable carriers comprising excipients

and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically for delivery to the site of action. Suitable formulations for parenteral administration include aqueous solutions of the active compounds in water soluble form, for example, water soluble salts. In addition, 5 suspensions of the active compounds as appropriate oily injection suspensions may be administered. Suitable lipophilic solvents or vehicles include fatty oils, for example, sesame oil, or synthetic fatty acid esters, for example, ethyl oleate or triglycerides. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension include, for example, sodium carboxymethyl cellulose, sorbitol, and/or dextran. 10 Optionally, the suspension may also contain stabilizers. Liposomes can also be used to encapsulate the agent for delivery into the cell.

The pharmaceutical formulation for systemic administration according to the invention may be formulated for enteral, parenteral or topical administration. Indeed, all three types of formulations may be used simultaneously to achieve systemic 15 administration of the active ingredient.

Suitable formulations for oral administration include hard or soft gelatin capsules, pills, tablets, including coated tablets, elixirs, suspensions, syrups or inhalations and controlled release forms thereof.

In practicing the methods of this invention, the compounds of this invention may 20 be used alone or in combination, or in combination with other therapeutic or diagnostic agents. In certain preferred embodiments, the compounds of this invention may be coadministered along with other compounds typically prescribed for these conditions according to generally accepted medical practice. The compounds of this invention can be utilized *in vivo*, ordinarily in mammals, such as humans, sheep, horses, cattle, pigs, dogs, 25 cats, rats and mice, or *in vitro*.

N. Rational Drug Design and Combinatorial Chemistry

The present invention further encompasses rational drug design and combinatorial chemistry. Those of skill will recognize appropriate methods to utilize and exploit aspects of the present invention in identifying compounds which can be developed for cancer treatment. Rational drug design involving polypeptides requires identifying and defining
5 a first peptide with which the designed drug is to interact, and using the first target peptide to define the requirements for a second peptide. With such requirements defined, one can find or prepare an appropriate peptide or non-peptide that meets all or substantially all of the defined requirements. Thus, one goal of rational drug design is to produce structural or functional analogs of biologically active polypeptides of interest or of small molecules
10 with which they interact (e.g., agonists, antagonists, null compounds) in order to fashion drugs that are, for example, more or less potent forms of the ligand. (See, e.g., Hodgson (1991), *Bio. Technology* 9:19-21). Combinatorial chemistry is the science of synthesizing and testing compounds for bioactivity en masse, instead of one by one, the aim being to discover drugs and materials more quickly and inexpensively than was formerly possible.
15 Rational drug design and combinatorial chemistry have become more intimately related in recent years due to the development of approaches in computer-aided protein modeling and drug discovery. (See e.g., US Pat. No. 4,908,773; 5,884,230; 5,873,052; 5,331,573; and 5,888,738).

The use of molecular modeling as a tool for rational drug design and combinatorial
20 chemistry has dramatically increased due to the advent of computer graphics. Not only is it possible to view molecules on computer screens in three dimensions but it is also possible to examine the interactions of macromolecules such as enzymes and receptors and rationally designed derivative molecules to test. (See Boorman (1992), *Chem. Eng. News* 70:18-26). A vast amount of user-friendly software and hardware is now available
25 and virtually all pharmaceutical companies have computer modeling groups devoted to rational drug design. Molecular Simulations Inc. (www.msi.com), for example, sells several sophisticated programs that allow a user to start from an amino acid sequence, build a two or three-dimensional model of the protein or polypeptide, compare it to other

two and three-dimensional models, and analyze the interactions of compounds, drugs, and peptides with a three dimensional model in real time. Accordingly, in some embodiments of the invention, software is used to compare regions of the invention protein and molecules that interact therewith (collectively referred to as "binding partners" —e.g., anti-
5 protein antibodies), and fragments or derivatives of these molecules with other molecules, such as peptides, peptidomimetics, and chemicals, so that therapeutic interactions can be predicted and designed. (See Schneider (1998), *Genetic Engineering News* December: page 20; Tempczyk *et al.* (1997), Molecular Simulations Inc. Solutions April; and Butenhof (1998), Molecular Simulations Inc. Case Notes (August 1998) for a discussion
10 of molecular modeling).

O. Gene Therapy

In another embodiment, genetic therapy can be used as a means for modulating biological and pathologic processes associated with the protein's function and activity. This comprises inserting into a cancerous cell a gene construct encoding a protein
15 comprising all or at least a portion of the sequences of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, or alternatively a gene construct comprising all or a portion of the non-coding region of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, operably linked to a promoter or enhancer element such that expression of said protein causes suppression of said cancer and wherein said promoter or enhancer element is a promoter or enhancer element
20 modulating said gene construct.

In the constructs described, expression of said protein can be directed from any suitable promoter (e.g., the human cytomegalovirus (CMV), simian virus 40 (SV40), or metallothionein promoters), and regulated by any appropriate mammalian regulatory element. For example, if desired, enhancers known to preferentially direct gene expression
25 in neural cells, T cells, or B cells may be used to direct the expression. The enhancers used could include, without limitation, those that are characterized as tissue or cell specific in their expression. Alternatively, if a genomic clone of LFG1, LFG2, LFG3, LFG4, LFG5

or LFG6 is used as a therapeutic construct (for example, following its isolation by hybridization with the nucleic acid molecule of the invention described above), regulation may be mediated by the cognate regulatory sequences or, if desired, by regulatory sequences derived from a heterologous source, including any of the promoters or regulatory elements described above.

Insertion of the construct into a cancerous cell is accomplished *in vivo*, for example using a viral or plasmid vector. Such methods can also be applied to *in vitro* uses. Thus, the methods of the present invention are readily applicable to different forms of gene therapy, either where cells are genetically modified *ex vivo* and then administered to a host or where the gene modification is conducted *in vivo* using any of a number of suitable methods involving vectors especially suitable to such therapies.

Retroviral vectors, adenoviral vectors, adeno-associated viral vectors, or other viral vectors with the appropriate tropism for cells likely to be involved in cancer (for example, epithelial cells) may be used as a gene transfer delivery system for a therapeutic gene construct. Numerous vectors useful for this purpose are generally known (Cozzi PJ, et al., (2002) *Prostate*, 53(2):95-100; Bitzer M, Lauer U., (2002) *Dtsch Med Wochenschr.* 127(31-32):1623-1624; Mezzina and Danos (2002), *Trends Genet.* 8:241-256; Loser et al. (2002) *Curr. Gene Ther.* 2:161-171; Pfeifer and Verma (2001), *Annu. Rev. Genomics Hum. Genet.* 2:177-211). Retroviral vectors are particularly well developed and have been used in clinical settings (Anderson et al. (1995), U.S. Patent No. 5,399,346). Non-viral approaches may also be employed for the introduction of therapeutic DNA into cells otherwise predicted to undergo cancer (Jeschke et al. (20002) *Curr. Gene Ther.* 1:267-278; Wu et al. (1988), *J. Biol. Chem.* 263:14621-14624; Wu et al. (1989), *J. Biol. Chem.* 264:16985-16987). For example, a gene may be introduced into a neuron or a T cell by lipofection, asialorosonucoid polylysine conjugation, or, less preferably, microinjection under surgical conditions.

For any of the methods of application described above, the therapeutic nucleic acid construct is preferably applied to the site of the cancer event (for example, by injection). However, it may also be applied to tissue in the vicinity of the cancer event or to a blood vessel supplying the cells predicted to undergo cancer.

5 P. Transgenic Animals

Transgenic animals containing mutant, knock-out or modified genes corresponding to the cDNA sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, or the open reading frame encoding the polypeptide sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, or fragments thereof having a consecutive sequence of at least about 3, 4, 5, 6, 10, 15, 20, 25,
10 30, 35 or more amino acid residues, are also included in the invention. Transgenic animals are genetically modified animals into which recombinant, exogenous or cloned genetic material has been experimentally transferred. Such genetic material is often referred to as a "transgene." The nucleic acid sequence of the transgene, in this case a form of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, may be integrated either at a locus of a
15 genome where that particular nucleic acid sequence is not otherwise normally found or at the normal locus for the transgene. The transgene may consist of nucleic acid sequences derived from the genome of the same species or of a different species than the species of the target animal.

In some embodiments, transgenic animals in which all or a portion of a gene comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 is deleted may be constructed. In those
20 cases where the gene corresponding to SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15 contains one or more introns, the entire gene- all exons, introns and the regulatory sequences- may be deleted. Alternatively, less than the entire gene may be deleted. For example, a single exon and/or intron may be deleted, so as to create an animal expressing a modified version
25 of a protein of the invention.

The term "germ cell line transgenic animal" refers to a transgenic animal in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring the ability of the transgenic animal to transfer the genetic information to offspring. If such offspring in fact possess some or all of that alteration or genetic information, then they too are transgenic animals.

The alteration or genetic information may be foreign to the species of animal to which the recipient belongs, foreign only to the particular individual recipient, or may be genetic information already possessed by the recipient. In the last case, the altered or introduced gene may be expressed differently than the native gene.

Transgenic animals can be produced by a variety of different methods including transfection, electroporation, microinjection, gene targeting in embryonic stem cells and recombinant viral and retroviral infection (*see, e.g.*, U.S. Patent No. 4,736,866; U.S. Patent No. 5,602,307; Mullins *et al.* (1993), *Hypertension* 22: 630-633; Brenin *et al.* (1997), *Surg. Oncol.* 6: 99-110; Recombinant Gene Expression Protocols (Methods in Molecular Biology, Vol. 62), Tuan, ed., Humana Press, Totowa, NJ, 1997).

A number of recombinant or transgenic mice have been produced, including those which express an activated oncogene sequence (U.S. Patent No. 4,736,866); express simian SV40 T-antigen (U.S. Patent No. 5,728,915); lack the expression of interferon regulatory factor 1 (IRF-1) (U.S. Patent No. 5,731,490); exhibit dopaminergic dysfunction (U.S. Patent No. 5,723,719); express at least one human gene which participates in blood pressure control (U.S. Patent No. 5,731,489); display greater similarity to the conditions existing in naturally occurring Alzheimer's disease (U.S. Patent No. 5,720,936); have a reduced capacity to mediate cellular adhesion (U.S. Patent No. 5,602,307); possess a bovine growth hormone gene (Clutter *et al.* (1996), *Genetics* 143: 1753-1760); or, are capable of generating a fully human antibody response (McCarthy (1997), *Lancet* 349: 405).

While mice and rats remain the animals of choice for most transgenic experimentation, in some instances it is preferable or even necessary to use alternative animal species. Transgenic procedures have been successfully utilized in a variety of non-murine animals, including sheep, goats, pigs, dogs, cats, monkeys, chimpanzees, hamsters, rabbits, cows and guinea pigs (see, *e.g.*, Kim *et al.* (1997), *Mol. Reprod. Dev.* 46: 515-526; Houdebine (1995), *Reprod. Nutr. Dev.* 35: 609-617; Petters (1994), *Reprod. Fertil. Dev.* 6: 643-645; Schnieke *et al.* (1997), *Science* 278: 2130-2133; and Amoah (1997), *J. Animal Sci.* 75: 578-585).

The method of introduction of nucleic acid fragments into recombination competent mammalian cells can be by any method which favors co-transformation of multiple nucleic acid molecules. Detailed procedures for producing transgenic animals are readily available to one skilled in the art, including the disclosures in U.S. Patent No. 5,489,743 and U.S. Patent No. 5,602,307.

Q. Diagnostic Methods

As the genes and proteins of the invention are differentially expressed in cancerous tissues compared to non-cancerous tissues, the genes and proteins of the invention may be used to diagnose or monitor cancer, to track disease progression, or to differentiate cancerous tissue from non-cancerous tissue samples. One means of diagnosing cancer using the nucleic acid molecules or proteins of the invention involves obtaining tissue from living subjects.

Assays to detect nucleic acid or protein molecules of the invention may be in any available format. Typical assays for nucleic acid molecules include hybridization or PCR based formats. Typical assays for the detection of proteins, polypeptides or peptides of the invention include the use of antibody probes in any available format such as *in situ* binding assays, etc. (see Harlow & Lane, Antibodies - A Laboratory Manual, Cold Spring

Harbor Laboratory Press, Cold Spring Harbor, NY, 1988). In preferred embodiments, assays are carried-out with appropriate controls.

Generally, the diagnostics of the invention can be classified according to whether the embodiment is a nucleic acid or protein-based assay. Some diagnostic assays detect mutations or polymorphisms in the invention nucleic acids or proteins, which contribute to cancerous aberrations. Other diagnostic assays identify and distinguish defects in protein activity by detecting a level of invention RNA or protein in a tested organism that resembles the level of invention RNA or protein in a organism suffering from a disease, such as cancer, or by detecting a level of RNA or protein in a tested organism that is different than an organism not suffering from a disease.

Additionally, the manufacture of kits that incorporate the reagents and methods described in the following embodiments so as to allow for the rapid detection and identification of aberrations in protein activity or level are contemplated. The diagnostic kits can include a nucleic acid probe or an antibody or combinations thereof, which specifically detect a mutant form of the invention protein or a nucleic acid probe or an antibody or combinations thereof, which can be used to determine the level of RNA or protein expression of one or more invention protein. The detection component of these kits will typically be supplied in combination with one or more of the following reagents. A support capable of absorbing or otherwise binding DNA, RNA, or protein will often be supplied. Available supports include membranes of nitrocellulose, nylon or derivatized nylon that can be characterized by bearing an array of positively charged substituents. One or more restriction enzymes, control reagents, buffers, amplification enzymes, and non-human polynucleotides like calf-thymus or salmon-sperm DNA can be supplied in these kits.

Useful nucleic acid-based diagnostic techniques include, but are not limited to, direct DNA sequencing, gradient gel electrophoresis, Southern Blot analysis, single-stranded confirmation analysis (SSCA), RNase protection assay, dot blot analysis, nucleic

acid amplification, allele-specific PCR and combinations of these approaches. The starting point for these analyses is isolated or purified nucleic acid from a biological sample. It is contemplated that tissue biopsies would provide a good sample source. The nucleic acid is extracted from the sample and can be amplified by a DNA amplification technique such as the Polymerase Chain Reaction (PCR) using primers. Those of skill in the art will readily recognize methods available for confirming the presence of polymorphisms. In addition, any addressable array technology known in the art can be employed with this aspect of the invention. One particular embodiment of polynucleotide arrays is known as GenechipsTM, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092.

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid assays. There are several ways to produce labeled nucleic acids for hybridization or PCR including, but not limited to, oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, a nucleic acid encoding an invention protein can be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3 or SP6 and labeled nucleotides. A number of companies such as Pharmacia Biotech (Piscataway, NJ), Promega (Madison, WI), and U.S. Biochemical Corp (Cleveland, OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as, substrates, cofactors, inhibitors, magnetic particles and the like.

In preferred protein-based diagnostic, antibodies of the invention are attached to a support in an ordered array wherein a plurality of antibodies are attached to distinct regions of the support that do not overlap with each other. Those of skill in the art will readily recognize available assays that are protein-based diagnostics. Proteins are obtained from biological samples and are labeled by conventional approaches (e.g.,

radioactivity, colorimetrically, or fluorescently). Employing labeled standards of a known concentration of mutant and/or wild-type invention protein, an investigator can accurately determine the concentration of the invention protein in a sample and from this information can assess the expression level of the particular form of the protein. Conventional methods
5 in densitometry can also be used to more accurately determine the concentration or expression level of such protein. These approaches are also easily automated using technology known to those of skill in the art of high throughput diagnostic analysis. As detailed above, any addressable array technology known in the art can be employed with this aspect of the invention and display the protein arrays on the chips in an attempt to
10 maximize antibody binding patterns and diagnostic information.

As discussed above, the presence or detection of a polymorphism in an invention gene or protein can provide a diagnosis of a cancer or similar malady in an organism. Additional embodiments include the preparation of diagnostic kits comprising detection components, such as antibodies, specific for a particular polymorphic variant of invention
15 gene or protein. The detection component will typically be supplied in combination with one or more of the following reagents. A support capable of absorbing or otherwise binding RNA or protein will often be supplied. Available supports for this purpose include, but are not limited to, membranes of nitrocellulose, nylon or derivatized nylon that can be characterized by bearing an array of positively charged substituents, and GenechipsTM or
20 their equivalents. One or more enzymes, such as Reverse Transcriptase and/or Taq polymerase, can be furnished in the kit, as can dNTPs, buffers, or non-human polynucleotides like calf-thymus or salmon-sperm DNA. Results from the kit assays can be interpreted by a healthcare provider or a diagnostic laboratory. Alternatively, diagnostic kits are manufactured and sold to private individuals for self-diagnosis.

25 In addition to diagnosing disease according to the presence or absence of a polymorphism, some diseases involving cancer result from skewed levels of invention protein or gene in particular tissues or aberrant patterns of invention protein expression. By monitoring the level of expression in various tissues, for example, a diagnosis can be

made or a disease state can be identified. Similarly, by determining ratios of the level of expression of various invention proteins in specific tissues (e.g., patterns of expression) a prognosis of health or disease can be made. The levels of invention protein expression in various tissues from healthy individuals, as well as, individuals suffering from cancers is
5 determined. These values can be recorded in a database and can be compared to values obtained from tested individuals. Additionally, the ratios or patterns of expression in various tissues from both healthy and diseased individuals is recorded in a database. These analyses are referred to as "disease state profiles" and by comparing one disease state profile (e.g. from a healthy or diseased individual) to a disease state profile from a tested
10 individual, a clinician can rapidly diagnose the presence or absence of disease.

The nucleic acid and protein-based diagnostic techniques described above can be used to detect the level or amount or ratio of expression of invention genes or proteins in a tissue. Through quantitative Northern hybridizations, *in situ* analysis, immunohistochemistry, ELISA, genechip array technology, PCR, and Western blots, for
15 example, the amount or level of expression of RNA or protein for a particular invention protein (wild-type or mutant) can be rapidly determined and from this information ratios of expression can be ascertained. Alternatively, the invention proteins to be analyzed can be family members that are currently unknown but which are identified based on their possession of one or more of the homology regions described above.

20 Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the
25 disclosure.

EXAMPLES

EXAMPLE 1: Identification of Differentially Expressed mRNA in Cancers - 1

Global changes in gene expression between tumor biopsies and normal tissues have been examined using the GeneExpress Oncology Datasuite™ of Gene Logic, Inc. (Gaithersburg, MD). The database includes the gene expression profiles, generated by
5 using the Affymetrix Human Genome U95 array, derived from normal and cancer tissue samples from many different organs. Among the tissue samples in the database, applicants analyzed the expression profiles of normal and cancer tissue sets from breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and stomach.

10 The Affymetrix Human Genome U95 array contains 63,175 probe sets. A probe set is a set of probes to detect one transcript (a gene or a cDNA clone), and usually consists of 16-20 oligonucleotide probe pairs. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of average difference. Average difference serves as a relative indicator of the level of expression of a
15 transcript and is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, an absolute call for each gene is made; "Absent"
20 (= not detected), "Present" (= detected) or "Marginal" (= not clearly Absent or Present).

Differential expression of genes between cancerous and normal tissue samples was determined with the following statistical methods. (1) For each probe set, average difference values and absolute calls were determined by Affymetrix Microarray Suite (v4.0). (2) In a given sample set, outliers among the tissue samples were detected by
25 Principal Component Analysis (PCA) using MatLab program (The MathWorks, Inc., Natick, MA). The data points used in the PCA were the average differences of randomly selected probe sets (5,000~6,000 probe sets). Outliers were excluded from further analysis.

(3) Variations of gene expression were analyzed by using the Fold Change Analysis tool of GeneExpress program. The fold change (cancerous/normal) was calculated by comparing the mean average difference for each gene in a cancerous sample set against the mean average difference of that gene in the normal tissue sample set. Genes showing at least 3-fold increases or decreases in expression level were obtained. Genes were included in the analysis if they had a p-value of less than or equal to 0.05 as determined by an Analysis of Variance Test (Steel *et al.*, Principles and Procedures of Statistics: A Biometrical Approach, Third Ed., McGraw-Hill, 1997). (4) Genes showing differential expression in at least 5 different cancer types were selected.

Analysis of the chip data showed that the expression of the marker LFG1 was significantly up-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG1 (SEQ ID NO: 1 or 3) can be measured by chip sequence fragment no. 91875_s_at on Affymetrix GeneChips® U95. The 91875_s_at sequence is derived from the EST AI053741. The expression levels of 91875_s_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 1, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold change greater than 1.5 was considered to be significant (Wodicka *et al.* (1997), *Nature Biotech.* 15:1359-1367). Also indicated in the Table 1 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that up-regulation of LFG1 may be diagnostic for cancer.

TABLE 1

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	22.71	34	8	4	22		
	INFILTRATING DUCT CARCINOMA	184.04	61	61	0	0	8.11 up	0
	INFILTRATING LOBULAR CARCINOMA	104.36	10	9	0	1	4.60 up	0.00456
COLON	NORMAL TISSUE, NOS	76.46	24	23	0	1		
	ADENOCARCINOMA, NOS	244.76	36	35	0	1	3.20 up	0.00001
	NORMAL TISSUE, NOS	50.47	18	16	1	1		
ESOPHAGUS	NORMAL TISSUE, NOS	297.56	8	8	0	0	5.90 up	0.00367
	ADENOCARCINOMA, NOS	20.00	25	1	0	24		
	NORMAL TISSUE, NOS	60.48	11	10	1	0	3.02 up	0.00082
KIDNEY	CLEAR CELL CARCINOMA	65.01	16	13	0	3	3.25 up	0.00011
	RENAL CELL CARCINOMA	22.06	19	3	0	16		
	NORMAL TISSUE, NOS	86.74	23	21	0	2	3.93 up	0
LIVER	HEPATOCELLULAR CARCINOMA, NOS	21.27	32	6	0	26		
	NORMAL TISSUE, NOS	122.81	39	38	0	1	5.77 up	0
	ADENOCARCINOMA, NOS	20.21	23	0	0	23		
OVARY	NORMAL TISSUE, NOS	112.80	23	21	0	2	5.58 up	0
	PAPILLARY SEROUS ADENOCARCINOMA	20.02	20	1	0	19		
	NORMAL TISSUE, NOS	72.55	25	22	0	3	3.62 up	0
PANCREAS	ADENOCARCINOMA, NOS	78.86	20	20	0	0		
	NORMAL TISSUE, NOS	259.95	22	22	0	0	3.30 up	0.00008
	ADENOCARCINOMA, NOS	36.06	18	7	0	11		
RECTUM	NORMAL TISSUE, NOS	218.74	38	36	0	2	6.07 up	0
	ADENOCARCINOMA, NOS							
	ADENOCARCINOMA, NOS							

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 91875_s_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GCTGAAGCAGGAAAATCGCTT-3' (SEQ ID NO: 17) and 5'-TGAGACGGAGTCTCACTCGGT-3' (SEQ ID NO: 18))
 5 designed based on the sequence information file of the specific Affymetrix fragment (91875_s_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-
 10 terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, kidney, liver, lung, ovary, stomach and pancreas (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the up-regulation of LFG1 in
 15 cancer compared to normal samples.

EXAMPLE 2: Cloning of Full-Length Human cDNA (LFG1) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 1 or 3 was obtained by polymerase chain reaction (PCR) and rapid amplification of cDNA ends (RACE) using cDNA library from
 20 human heart (ResGen, Huntsville, AL). Gene-specific oligos for PCR (5'-CACCCTTTGCCTCTGTCACTTCCGCA-3' (SEQ ID NO: 21), 5'-GCTGGAGCACCAGGACTGCATTG-3' (SEQ ID NO: 22), 5'-GGAGCTGAGCAGCAGTGTAATGAA-3' (SEQ ID NO: 23), 5'-GAGGCCTGCCTGAAGGAGGAGCTTC-3' (SEQ ID NO: 24), 5'-
 25 TCTGGAAGTAGTGCAGACGCCTCAGG-3' (SEQ ID NO: 25), 5'-AGCCAACGTCGGCTTTGTTATCCAGC-3' (SEQ ID NO: 26), 5'-

GCTGTCAGATATGATGGTTCTGGAC-3' (SEQ ID NO: 27), 5'-
 CCAGCCTCACCCTGTTGGGTTGC-3' (SEQ ID NO: 28), 5'-
 CATTCTCTGAGCTGTATTAGTGT-3' (SEQ ID NO: 29), 5'-
 CCTGAGCTGGAATGACCTGCA-3' (SEQ ID NO: 30), 5'-
 5 CTTTGTGTTGGCTGCAGCCACA-3' (SEQ ID NO: 31), 5'-
 TGAGGAGAGACTTTGCTGACTGGT-3' (SEQ ID NO: 32), 5'-
 GTCCTGTCTGGCGGTGCCGA-3' (SEQ ID NO: 33), 5'-
 GCTCCAGGATCCCCTGTCACCTGGGCCTTCTGCCTTTTGGCT-3' (SEQ ID NO: 34),
 5'-CCATATGGAGAGGAGAGCAGCGGGCCCA-3' (SEQ ID NO: 35), 5'-
 10 GAAGGAGGAACATGGAGAGGAGA-3' (SEQ ID NO: 36), 5'-
 CCATATGCCCCGGGTAGTCTACTGCAT-3' (SEQ ID NO: 37), and 5'-
 GTCGACTCGAGTCACTTCCGCAAAAACCTTCTTG-3' (SEQ ID NO: 38)) and RACE
 (5'-TCCATTCCGAAGGCTCTCCTCC-3' (SEQ ID NO: 39), 5'-
 GTCTGTGTGACGGAAATGTAAGC-3' (SEQ ID NO: 40), and 5'-
 15 GAAGGTCGAAGGCAGACCGATGT-3' (SEQ ID NO: 41)) were designed based on
 predicted genes containing the 91875_s_at sequence using Human Genome Browser
 (University of California, Santa Cruz). The amplified products with the primers were
 incorporated into PCR4-Topo vector using Topo Cloning System (Invitrogen, Carlsbad,
 CA), and followed by sequencing.

20 The nucleotide sequence of the full-length human cDNAs corresponding to the
 differentially regulated mRNA detected above is set forth in SEQ ID NOS: 1 and 3. In the
 former, the cDNA comprises 5293 base pairs. In the latter, the cDNA comprises 5317 base
 pairs.

25 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 1, at
 nucleotides 390-4880 (390-4883 including the stop codon), encodes a protein of 1497
 amino acids. The amino acid sequence corresponding to a predicted protein encoded by
 SEQ ID NO: 1 is set forth in SEQ ID NO: 2. Figure 2 shows the results of a hydrophobicity

analysis of the amino acid sequence of SEQ ID NO: 2 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

5 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 3, at nucleotides 12-4904 (12-4907 including the stop codon), encodes a protein of 1631 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 3 is set forth in SEQ ID NO: 4. Figure 3 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 4 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce
10 antigenic peptides, as described above.

The protein sequence of SEQ ID NO: 2 is identical to that of SEQ ID NO: 4, except that SEQ ID NO: 2 lacks the first 134 amino acids at the N-terminus of SEQ ID NO: 4.

SEQ ID NOS: 2 and 4 contain Calponin homology domain (amino acid positions 38-145 of SEQ ID NO: 4), IQ domain for calmodulin-binding (amino acid positions 629-646 of
15 SEQ ID NO: 2 and amino acid positions 763-780 of SEQ ID NO: 4), RasGAP domain (amino acid positions 858-1195 of SEQ ID NO: 2 and amino acid positions 992-1329 of SEQ ID NO: 4), and RasGAP C-terminal domain (amino acid positions 1298-1421 of SEQ ID NO: 2 and amino acid positions 1432-1555 of SEQ ID NO: 4). SEQ ID NOS: 2 and 4 are similar to IQGAP proteins (Weissbach *et al.* (1994), *J Biol Chem* 269:20517-20521;
20 Brill *et al.* (1996), *Mol Cell Biol* 16:4869-4878). IQGAP binds to and modulate the function of proteins involved in cytoskeletal structure, cell-cell adhesion, and proliferation signaling (Fukada *et al.* (2002), *Cell* 109: 1-20; Briggs *et al.* (2002), *J Biol Chem* 277: 7453-7465; McCallum *et al.* (1998), *J Biol Chem* 273: 22537-22544). IQGAP1-deficient mice exhibited a significant increase in late-onset gastric hyperplasia relative to wild-type (Li *et al.* (2000), *Mol Cell Biol* 20: 697-701).
25

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG1. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and an EST containing 91875_s_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed three transcripts for this gene, which are approximately 7.2 kb, and 6.3 kb in size. This corresponds to the sizes of the LFG1 clones (SEQ ID NO: 1 and 3).

10 EXAMPLE 3: Identification of Differentially Expressed mRNA in Cancers - 2

The process in EXAMPLE 1 was repeated except that the marker LFG2 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG2 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG2 (SEQ ID NO: 5) can be measured by chip sequence fragment no. 82941_at on Affymetrix GeneChips® U95. The 82941_at sequence is derived from the EST AI277612. The expression levels of 82941_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 2, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the Table 2 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG2 may be diagnostic for cancer.

TABLE 2

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	1147.66	34	34	0	0		
	INFILTRATING DUCT CARCINOMA	129.77	61	26	3	32	8.71 down	0
	INFILTRATING LOBULAR CARCINOMA	183.37	10	6	1	3	5.48 down	0.00002
COLON	NORMAL TISSUE, NOS	890.08	24	23	1	0		
	ADENOCARCINOMA, NOS	163.35	36	17	1	18	5.39 down	0
	NORMAL TISSUE, NOS	612.34	18	18	0	0		
ESOPHAGUS	ADENOCARCINOMA, NOS	265.11	8	7	1	0	2.31 down	0.02218
	NORMAL TISSUE, NOS	182.73	19	11	1	7		
	HEPATOCELLULAR CARCINOMA, NOS	114.69	23	7	1	15	1.51 down	0.01211
LUNG	NORMAL TISSUE, NOS	535.64	32	30	2	0		
	ADENOCARCINOMA, NOS	119.36	39	17	3	19	4.27 down	0
	NORMAL TISSUE, NOS	454.08	9	7	0	2		
LYMPH NODE	MALIGNANT LYMPHOMA, NOS	123.13	12	5	0	7	3.24 down	0.02245
	NORMAL TISSUE, NOS	279.99	23	21	0	2		
	PAPILLARY SEROUS ADENOCARCINOMA	85.45	23	7	1	15	3.5 down	0
PROSTATE	NORMAL TISSUE, NOS	185.77	19	13	1	5		
	ADENOCARCINOMA, NOS	80.06	19	2	2	15	2.57 down	0.00011
	NORMAL TISSUE, NOS	943.86	20	19	0	1		
RECTUM	ADENOCARCINOMA, NOS	176.45	22	13	2	7	5.2 down	0
	NORMAL TISSUE, NOS	414.40	18	16	0	2		
	ADENOCARCINOMA, NOS	125.39	38	17	2	19	3.21 down	0

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 82941_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GAATGTGTCAGAGACAAGTGCAGC-3' (SEQ ID NO: 42) and 5'-TGTAGAACTCTTGGACTAATGGAGG-3' (SEQ ID NO: 43)) designed based on the sequence information file of the EST containing the Affymetrix fragment (82941_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, liver, lung, ovary, and stomach (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG2 in cancer compared to normal samples.

EXAMPLE 4: Cloning of Full-Length Human cDNA (LFG2) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 5 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GAATGTGTCAGAGACAAGTGCAGC-3' (SEQ ID NO: 42)) was designed based on the sequence of the EST containing 82941_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a poorly differentiated stomach adenocarcinoma library (NCI CGAP Gas4) (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating.

The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

5 The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 5. The cDNA comprises 3608 base pairs.

 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 5, at nucleotides 424-1908 (424-1911 including the stop codon), encodes a protein of 495 amino
10 acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 5 is set forth in SEQ ID NO: 6.

 SEQ ID NO: 6 has homology to scavenger receptors, which are involved in endocytosis of selected polyanionic ligands, phagocytosis of apoptotic cells and bacteria, cell adhesion, and development of atherosclerosis (Peiser *et al.* (2002), *Curr. Opin.*
15 *Immunol.* 14:123-128; Resnick *et al.* (1994), *Trends Biol. Sci.* 19:5-8). Based on published studies of scavenger receptors, SEQ ID NO: 6 contains a cytoplasmic domain (amino acid positions 1-35), a transmembrane domain (amino acid positions 36-58), an α -helical coiled-coil domain (amino acid positions 90-301), a collagen-like domain (amino acid positions 305-380), and a scavenger receptor cystein-rich (SRCR) domain (amino acid positions 393-
20 493). The SRCR domain contains six cysteine residues (amino acid positions 418, 431, 462, 472, 482, and 492), which may participate in intradomain disulfide bonds. SEQ ID NO: 6 also exhibits homology to a mouse homologue (GenBank Accession No. BC016096). It shows 70% identity over the entire contiguous sequence.

 Figure 4 shows the results of a hydrophobicity analysis of the amino acid sequence
25 of SEQ ID NO: 6 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.*

157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG2. A Northern blot containing total RNAs from various human tissues was used (Human MTN Blot, Clontech, Palo Alto, CA), and the EST containing 82941_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 3.7 kb in size. This corresponds to the size of the LFG2 clone (SEQ ID NO: 5).

EXAMPLE 5: Identification of Differentially Expressed mRNA in Cancers - 3

The process in EXAMPLE 1 was repeated except that the marker LFG3 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG3 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG3 (SEQ ID NO: 7) can be measured by chip sequence fragment no. 46104_at on Affymetrix GeneChips® U95. The 46104_at sequence is derived from the EST AA772055. The expression levels of 46104_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 3, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the

Table 3 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG3 may be diagnostic for cancer.

TABLE 3

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	64.52	34	31	0	3		
	INFILTRATING DUCT CARCINOMA	27.24	61	18	1	42	down	0
	INFILTRATING LOBULAR CARCINOMA	29.52	10	4	0	6	down	0.00004
COLON	NORMAL TISSUE, NOS	315.46	24	24	0	0		
	ADENOCARCINOMA, NOS	102.99	36	31	0	5	down	0.00016
ESOPHAGUS	NORMAL TISSUE, NOS	272.48	18	17	0	1		
	ADENOCARCINOMA, NOS	41.25	8	6	0	2	down	0.00001
KIDNEY	NORMAL TISSUE, NOS	2626.88	25	25	0	0		
	CLEAR CELL ADENOCARCINOMA, NOS	344.66	11	11	0	0	down	0.00003
	RENAL CELL CARCINOMA	355.71	16	14	0	2	down	0.00005
OVARY	NORMAL TISSUE, NOS	1098.41	23	23	0	0		
	PAPILLARY SEROUS ADENOCARCINOMA	178.15	23	22	0	1	down	0
	NORMAL TISSUE, NOS	274.49	19	19	0	0		
PROSTATE	ADENOCARCINOMA, NOS	117.26	19	18	0	1	down	0.00016
	NORMAL TISSUE, NOS	410.22	20	20	0	0		
RECTUM	ADENOCARCINOMA, NOS	72.98	22	16	0	6	down	0
	NORMAL TISSUE, NOS	71.10	18	10	0	8		
STOMACH	NORMAL TISSUE, NOS	35.49	38	15	1	22	down	0.00459
	ADENOCARCINOMA, NOS							

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 46104_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GTATGCATCAGAATTCCCTATAGATCTTT-3' (SEQ ID NO: 44) and 5'-TAGATGTTTGGGCAACAGCCT-3' (SEQ ID NO: 45)) designed based on the sequence information file of the EST containing the Affymetrix fragment (46104_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, kidney, ovary, pancreas, and stomach (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG3 in cancer compared to normal samples.

EXAMPLE 6: Cloning of Full-Length Human cDNA (LFG3) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 7 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GTATGCATCAGAATTCCCTATAGATCTTT-3' (SEQ ID NO: 44)) was designed based on the sequence of the EST containing 46104_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from human fetal kidney (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was

screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing. The 5'-end of LFG3 was identified by rapid amplification of cDNA ends (RACE) using the cDNA prepared from human fetal kidney (Clontech, Palo Alto, CA) and a gene specific primer (5'-
 5 TTCCTTCACCAAAGGCATCCAGCCATTCTATG-3' (SEQ ID NO: 46)).

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 7. The cDNA comprises 3162 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 7, at
 10 nucleotides 405-1835 (405-1838 including the stop codon), encodes a protein of 477 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 7 is set forth in SEQ ID NO: 8.

SEQ ID NO: 8 is similar to monocarboxylate transporters (MCTs) and contains ten predicted transmembrane domains (amino acids positions 10-29, 80-99, 107-128, 140-160,
 15 274-295, 312-332, 339-360, 363-384, 396-416, and 433-451). MCT proteins catalyze the facilitated transport of monocarboxylates such as lactate, pyruvate, branched-chain oxo acids, ketone bodies, beta-hydroxy-butylate, and acetate (Halestrap and Price (1999), *Biochem. J.* 343:281-299). Table 4 summarizes the similarity ratios of SEQ ID NO: 4 with the eight known monocarboxylate transporters.

20

TABLE 4. Homology of LFG3 with MCT proteins

Protein	Size (amino acids)	Identity (%)	Positives (%)
MCT1	500	17.5	34.3
MCT2	478	19.5	35.5
MCT3	504	19.5	34.1
MCT4	465	19.0	33.2

MCT5	487	22.1	36.9
MCT6	505	16.4	31.5
MCT7	523	20.1	35.2
MCT8	613	15.9	27.9

Figure 5 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 8 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG3. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and the EST containing 46104_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 4.2 kb in size. This corresponds to the size of the LFG3 clone (SEQ ID NO: 7).

EXAMPLE 7: Identification of Differentially Expressed mRNA in Cancers - 4

The process in EXAMPLE 1 was repeated except that the marker LFG4 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG4 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG4 (SEQ ID NO: 9) can be measured by chip sequence fragment no. 62158_at on Affymetrix GeneChips® U95. The 622158_at sequence is derived from the EST AI123532. The expression levels of 62158_at in various malignant

neoplasms, compared to normal control tissues, are shown in Table 5, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold-change greater than 1.5 was considered to be significant (Wodicka et al. (1997), Nature Biotech. 15:1359-1367). Also indicated in the Table 5 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that down-regulation of LFG4 may be diagnostic for cancer.

TABLE 5

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal	Absent		
BREAST	NORMAL TISSUE, NOS	156.75	34	33	0	1		
	INFILTRATING DUCT CARCINOMA	90.09	61	51	0	10	1.74 down	0.00001
COLON	NORMAL TISSUE, NOS	234.06	24	22	2	0		
	ADENOCARCINOMA, NOS	64.02	36	24	0	12	3.66 down	0
KIDNEY	NORMAL TISSUE, NOS	134.17	25	23	0	2		
	CLEAR CELL ADENOCARCINOMA, NOS	78.59	11	7	1	3	1.71 down	0.08272
LUNG	RENAL CELL CARCINOMA	55.31	16	9	0	7	2.43 down	0.0021
	NORMAL TISSUE, NOS	179.71	32	32	0	0		
LYMPH NODE	ADENOCARCINOMA, NOS	47.39	39	17	3	19	3.79 down	0
	NORMAL TISSUE, NOS	140.51	9	7	1	1		
OVARY	MALIGNANT LYMPHOMA, NOS	41.43	12	5	1	6	3.39 down	0.00207
	NORMAL TISSUE, NOS	125.19	23	21	0	2		
PROSTATE	PAPILLARY SEROUS ADENOCARCINOMA	37.23	23	4	0	19	3.36 down	0
	NORMAL TISSUE, NOS	191.94	19	18	0	1		
RECTUM	ADENOCARCINOMA, NOS	103.47	19	16	0	3	1.86 down	0.00185
	NORMAL TISSUE, NOS	317.95	20	20	0	0		
STOMACH	ADENOCARCINOMA, NOS	74.28	22	16	1	5	4.28 down	0
	NORMAL TISSUE, NOS	161.77	18	17	0	1		
	ADENOCARCINOMA, NOS	84.55	38	27	2	9	1.91 down	0.0062

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 62158_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-AAATGTCTGATTACCCCATTTTATCAGT-3' (SEQ ID NO: 47) and 5'-TAATCCTGAAATGAACAGCTAACA-3') (SEQ ID NO: 48) designed based on the sequence information file of the EST containing the Affymetrix fragment (62158_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from colon, liver, lung, ovary, pancreas, and stomach (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the down-regulation of LFG4 in cancer compared to normal samples.

EXAMPLE 8: Cloning of Full-Length Human cDNA (LFG4) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 9 was obtained by rapid amplification of cDNA ends (RACE). Briefly, gene-specific oligos (5'-TAATGTTAGAGTAACAGCATTTTCCTTCAA-3' (SEQ ID NO: 49) and 5'-TGCCCCACACTAACTCAGTTCTTGTGATG-3' (SEQ ID NO: 50)) were designed based on the sequence of the EST containing 62158_at sequence. The oligos was used for PCR amplification of the cDNAs prepared from human brain (Clontech, Palo Alto, CA). The amplified products with the primers were incorporated into PCR4-Topo vector using Topo Cloning System (Invitrogen, Carlsbad, CA), and followed by sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 9. The cDNA comprises 4891 base pairs.

5 An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 9, at nucleotides 89-1150 (89-1153 including the stop codon), encodes a protein of 354 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 9 is set forth in SEQ ID NO: 10.

10 SEQ ID NO: 10 is similar to rat Kilon and chicken Neurotractin (Funatsu *et al.* (1999), *J Biol Chem* 274:8224-8230; Marg *et al.* (1999), *J Cell Biol* 145:865-876). Protein sequence analysis reveals a secretory signal peptide (amino acid positions 1-33), three immunoglobulin domains (amino acid positions 47-136, 145-208, and 231-312), and six putative *N*-linked glycosylation sites (amino acid positions 73, 155, 275, 286, 294, and 307). Kilon/Neurotractin is a member of IgLON subfamily of the immunoglobulin superfamily. IgLONs are a family of glycosylphosphatidylinositol (GPI)-linked cell adhesion molecules
15 which are thought to modify neurite outgrowth and might play a role in cell-cell adhesion and recognition (Miyate *et al.* (2000), *J Comparative Neurol* 424:74-85).

Figure 6 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 10 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described
20 above. This hydropathy plot shows the presence of hydrophobic region at the C-terminus. In case of GPI-anchored proteins, the addition of the GPI anchor is known to occur after the cleavage of the C-terminal hydrophobic region. A putative GPI anchor attachment site was found (Gly at the amino acid position 324).

Analysis by Northern blot was performed to determine the size of the mRNA
25 transcripts that correspond to LFG4. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and the

EST containing 62158_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single
5 transcript for this gene, which is approximately 5.4 kb in size. This corresponds to the size of the LFG4 clone (SEQ ID NO: 9).

EXAMPLE 9: Identification of Differentially Expressed mRNA in Cancers - 5

The process in EXAMPLE 1 was repeated except that the marker LFG5 was used instead of the marker LFG1.

10 Analysis of the chip data showed that the expression of the marker LFG5 was significantly down-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG5 (SEQ ID NO: 11) can be measured by chip sequence fragment no. 46659_at on Affymetrix GeneChips® U95. The expression levels of 46659_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 6,
15 where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. Also indicated in the Table 6 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together
20 with the total number of samples in that sample set. These data indicate that differential regulation of LFG5 may be diagnostic for cancer.

TABLE 6

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal / Absent			
BREAST	NORMAL TISSUE, NOS	152.75	34	31	0	3		
	INFILTRATING DUCT CARCINOMA	404.58	61	60	0	1	2.65 up	0
	INFILTRATING LOBULAR CARCINOMA	277.71	10	10	0	0	1.82 up	0.07445
ESOPHAGUS	NORMAL TISSUE, NOS	85.47	18	15	0	2		
	ADENOCARCINOMA, NOS	373.97	8	8	0	0	4.38 up	0.0009
KIDNEY	NORMAL TISSUE, NOS	53.58	25	17	0	8		
	CLEAR CELL CARCINOMA	161.36	11	11	0	0	3.01 up	0.00011
	RENAL CELL CARCINOMA	249.37	16	16	0	0	4.65 up	0
	NORMAL TISSUE, NOS	330.65	32	31	0	1		
LUNG	ADENOCARCINOMA, NOS	195.43	39	35	0	4	1.69 down	0.00538
	NORMAL TISSUE, NOS	219.77	9	9	0	0		
LYMPH NODE	NORMAL TISSUE, NOS	142.09	12	11	0	1	1.55 down	0.25114
	MALIGNANT LYMPHOMA, NOS	90.40	23	19	0	4		
OVARY	NORMAL TISSUE, NOS	418.81	23	23	0	0	4.63 up	0
	PAPILLARY SEROUS ADENOCARCINOMA	38.53	20	12	0	8		
PANCREAS	NORMAL TISSUE, NOS	344.37	25	25	0	0	8.94 up	0
	ADENOCARCINOMA, NOS	185.50	18	17	0	1		
STOMACH	NORMAL TISSUE, NOS	279.62	38	35	0	3	1.51 up	0.12664
	ADENOCARCINOMA, NOS							

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 46659_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-AAGGCTTTATCAGGTCTGCATATAGAATC-3' (SEQ ID NO: 51) and 5'-GCAAAGAACCCTAATGCTATTTATCAGC-3' (SEQ ID NO: 52)) designed based on the sequence information file of the specific Affymetrix fragment (46659_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from kidney, lung, ovary, and pancreas (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the differential regulation of LFG5 in cancer compared to normal samples.

EXAMPLE 10: Cloning of Full-Length Human cDNA (LFG5) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 11 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-GAGAAGACCAGGGAAGAAGCAG-3' (SEQ ID NO: 53)) was designed based on the sequence of an EST containing 46659_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a human heart library (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and the longest cDNA was

screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NO: 11. The cDNA
5 comprises 3098 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 11, at nucleotides 223-1569 (223-1572 including the stop codon), encodes a protein of 449 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 11 is set forth in SEQ ID NO: 12.

10 SEQ ID NO: 12 contains a thymidylate kinase domain (amino acid positions 257-438). Thymidylate kinase is a member of nucleotide monophosphate kinases (NMPKs) which play roles in the nucleotide synthesis for RNA and DNA synthesis and are required for the pharmacological activation of therapeutic nucleoside and nucleotide analogs (Van Rompay *et al.* (2000), *Pharmacology & Therapeutics* 87:189-198). SEQ ID NO: 12 exhibits
15 homology to a mouse thymidylate kinase (GenBank Accession No. NM_020557) which is induced during macrophage activation (Lee and O'Brien (1995), *J Immunol.* 154:6094-6102). It shows 63% identity over the entire contiguous sequence.

Figure 7 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 12 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.*
20 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG5. A Northern blot containing total RNAs from various human tissues was used (Human MTN Blot, Clontech, Palo Alto, CA), and an EST
25 containing 82941_at sequence was radioactively labeled by the random primer method and

used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed a single transcript for this gene, which is approximately 3.0 kb in size. This corresponds to the size of the LFG5 clone (SEQ ID NO: 11).

EXAMPLE 11: Identification of Differentially Expressed mRNA in Cancers - 6

The process in EXAMPLE 1 was repeated except that the marker LFG6 was used instead of the marker LFG1.

Analysis of the chip data showed that the expression of the marker LFG6 was significantly up-regulated in cancer tissue samples compared to samples from normal tissue. The expression level of LFG6 (SEQ ID NO: 13 or 15) can be measured by chip sequence fragment no. 44103_at on Affymetrix GeneChips® U95. The 44103_at sequence is derived from the EST AA865614. The expression levels of 44103_at in various malignant neoplasms, compared to normal control tissues, are shown in Table 7, where the fold-change, the direction of the change (up- or down-regulation), p-value are also indicated. The fold change (cancerous/normal) was calculated by comparing the geometric mean of average difference in a cancerous sample set against the geometric mean of average difference in the normal tissue sample set. A fold change greater than 1.5 was considered to be significant (Wodicka *et al.* (1997), *Nature Biotech.* 15:1359-1367). Also indicated in the Table 7 are, for each tissue type, the numbers of samples that are called present, absent, or marginal together with the total number of samples in that sample set. These data indicate that up-regulation of LFG6 may be diagnostic for cancer.

TABLE 7

Tissue	Pathology / Morphology	Geometric Mean	Number of Samples			Fold Change	Direction	p-value
			Total	Present	Marginal / Absent			
KIDNEY	NORMAL TISSUE, NOS	337.71	25	25	0			
	CLEAR CELL ADENOCARCINOMA, NOS	556.82	11	11	0	1.65	up	0.00314
LIVER	NORMAL TISSUE, NOS	406.93	19	18	0			
	HEPATOCELLULAR CARCINOMA, NOS	619.40	23	22	0	1.52	up	0.00303
OVARY	NORMAL TISSUE, NOS	380.10	23	23	0			
	PAPILLARY SEROUS ADENOCARCINOMA	578.60	23	23	0	1.52	up	0.00013
PANCREAS	NORMAL TISSUE, NOS	138.75	20	11	1			
	ADENOCARCINOMA, NOS	453.01	25	25	0	3.26	up	0.00002

The GeneChip expression results, determined by sample binding to chip sequence fragment no. 44103_at, were validated by quantitative RT-PCR (Q-RT-PCR) using the Taqman® assay (Perkin-Elmer). PCR primers (5'-GGACGGGGAAGTGGACGC-3' (SEQ ID NO: 54) and 5'-AAGTGCAGGGCCTCTGGGTG-3' (SEQ ID NO: 55)) designed
5 based on the sequence information file of the specific Affymetrix fragment (44103_at) were used in the assay. The target gene in each RNA sample (10 ng of total RNA) was assayed relative to a reference gene. For this purpose, primers (5'-GTTTTTCCTAATTTTGGCATGAAC-3' (SEQ ID NO: 19) and 5'-CGCCCAAGCTTTTCCTTTT-3' (SEQ ID NO: 20)) specific to the CTBP1 gene (C-
10 terminal binding protein 1) were used to serve as control primers. This approach provides the relative expression as measured by cycle threshold (Ct) value of the target mRNA relative to an amount of CTBP1 Ct value. The sample panel included total RNA pairs of normal and tumor tissues from liver and ovary (Ambion, Inc., Austin, TX). The Q-RT-PCR data confirms the up-regulation of LFG6 in cancer compared to normal samples.

15 EXAMPLE 12: Cloning of Full-Length Human cDNA (LFG6) Corresponding to Differentially Expressed mRNA Species

The full-length cDNA having SEQ ID NO: 13 or 15 was obtained by the oligo-pulling method using the GeneTrapper assay (Life Technologies, Rockville, MD). Briefly, a gene-specific oligo (5'-CGCTGGGTCATCGGACGGT-3' (SEQ ID NO: 56)) was
20 designed based on the sequence of an EST containing 44103_at sequence. The oligo was labeled with biotin and used to hybridize with 5 µg of single strand plasmid DNA (cDNA recombinants) from a fully differentiated human stomach adenocarcinoma library (ResGen, Huntsville, AL) following the procedures of Sambrook *et al.* The hybridized cDNAs were separated by streptavidin-conjugated beads and eluted by heating. The eluted cDNA was
25 converted to double strand plasmid DNA and used to transform *E. coli* cells (DH10B) and

the longest cDNA was screened. After positive selection was confirmed by PCR using gene-specific primers, the cDNA clone was subjected to DNA sequencing.

The nucleotide sequence of the full-length human cDNAs corresponding to the differentially regulated mRNA detected above is set forth in SEQ ID NOS: 13 and 15. In the former, the cDNA comprises 1893 base pairs. In the latter, the cDNA comprises 1597 base pairs.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 13, at nucleotides 418-1392 (418-1395 including the stop codon), encodes a protein of 325 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 13 is set forth in SEQ ID NO: 14. Figure 9 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 14 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

An open reading frame within the cDNA nucleotide sequence of SEQ ID NO: 15, at nucleotides 271-1431 (271-1434 including the stop codon), encodes a protein of 387 amino acids. The amino acid sequence corresponding to a predicted protein encoded by SEQ ID NO: 15 is set forth in SEQ ID NO: 16. Figure 10 shows the results of a hydrophobicity analysis of the amino acid sequence of SEQ ID NO: 16 using Kyte-Doolittle values (Kyte and Doolittle (1982), *J. Mol. Biol.* 157:105-142). Hydrophilic regions may be used to produce antigenic peptides, as described above.

SEQ ID NOS: 14 and 16 contain ubiquitin homologues (UBQ) domain (amino acid positions 239-300). SEQ ID NOS: 14 and 16 are similar to rat Sharpin protein (Lim *et al.* (2001), *Mol Cell Neurosci* 17:385-397). Sharpin directly interacts with the ankyrin repeats of Shank protein which functions in the organization of cytoskeletal complexes and intracellular signaling at specialized cell junctions (Sheng and Kim (2000), *J Cell Sci* 113:1851-1856).

Analysis by Northern blot was performed to determine the size of the mRNA transcripts that correspond to LFG6. A Northern blot containing total RNAs from various human tissues was used (Human 12-Lane MTN Blot, Clontech, Palo Alto, CA), and an EST containing 44103_at sequence was radioactively labeled by the random primer method and used to probe the blot. The blot was hybridized in 50% formamide, 5X SSPE, 0.1% SDS, 5X Denhart's solution, and 0.2 mg/ml herring sperm DNA at 42°C and washed with 0.2X SSC containing 0.1% SDS at room temperature. The Northern blot showed three transcripts for this gene, which are approximately 2.2 kb, 1.5 kb, and 1.2 kb in size. This corresponds to the sizes of the LFG6 clones (SEQ ID NO: 13 and 15).

Although the present invention has been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents, patent applications and publications referred to in this application are herein incorporated by reference in their entirety.

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule selected from the group consisting of: (a) an isolated nucleic acid molecule comprising SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, (b) an isolated nucleic acid molecule encoding SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, (c) an isolated nucleic acid molecule that encodes a protein that is expressed in cancer and that exhibits at least about 75% nucleotide sequence identity over the entire contiguous sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13 or 15, and (d) an isolated nucleic acid molecule comprising the complement of a nucleic acid molecule of (a), (b) or (c).
2. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises nucleotides 390-4880 of SEQ ID NO: 1, nucleotides 12-4904 of SEQ ID NO: 3, nucleotides 424-1908 of SEQ ID NO: 5, nucleotides 405-1835 of SEQ ID NO: 7, nucleotides 89-1150 of SEQ ID NO: 9, nucleotides 223-1569 of SEQ ID NO: 11, nucleotides 418-1392 of SEQ ID NO: 13, or nucleotides 271-1431 of SEQ ID NO: 15.
3. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises nucleotides 390-4883 of SEQ ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1911 of SEQ ID NO: 5, nucleotides 405-1838 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1572 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, or nucleotides 271-1434 of SEQ ID NO: 15.
4. The isolated nucleic acid molecule of claim 1, wherein the nucleic acid molecule consists of nucleotides 390-4883 of SEQ ID NO: 1, nucleotides 12-4907 of SEQ ID NO: 3, nucleotides 424-1908 of SEQ ID NO: 5, nucleotides 405-1835 of SEQ ID NO: 7, nucleotides 89-1153 of SEQ ID NO: 9, nucleotides 223-1569 of SEQ ID NO: 11, nucleotides 418-1395 of SEQ ID NO: 13, or nucleotides 271-1434 of SEQ ID NO: 15.
5. The isolated nucleic acid molecule of any one of claims 1-4, wherein said nucleic acid molecule is operably linked to one or more expression control elements.

6. A vector comprising an isolated nucleic acid molecule of any one of claims 1-4.

7. A host cell transformed to contain the nucleic acid molecule of any one of claims 1-4.

5 8. A host cell comprising a vector of claim 6.

9. A host cell of claim 8, wherein said host cell is selected from the group consisting of prokaryotic host cells and eukaryotic host cells.

10 10. A method for producing a polypeptide comprising culturing a host cell transformed with the nucleic acid molecule of any one of claims 1-4 under conditions in which the protein encoded by said nucleic acid molecule is expressed.

11. The method of claim 10, wherein said host cell is selected from the group consisting of prokaryotic host cells and eukaryotic host cells.

12. An isolated polypeptide produced by the method of claim 10.

15 13. An isolated polypeptide or protein selected from the group consisting of a protein comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16, and a protein having at least about 75% amino acid sequence identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

14. An isolated antibody or antigen-binding antibody fragment that binds to a polypeptide of claim 13.

20 15. An antibody of claim 14 wherein said antibody is a monoclonal or a polyclonal antibody.

16. A method of identifying an agent which modulates the expression of a nucleic acid encoding a protein of claim 13, comprising:

exposing cells which express the nucleic acid to the agent; and

determining whether the agent modulates expression of said nucleic acid, thereby identifying an agent which modulates the expression of a nucleic acid encoding the protein.

- 5 17. A method of identifying an agent which modulates the level of or at least one activity of a protein of claim 13, comprising:

exposing cells which express the protein to the agent;

- 10 determining whether the agent modulates the level of or at least one activity of said protein, thereby identifying an agent which modulates the level of or at least one activity of the protein.

18. The method of claim 17, wherein the agent modulates one activity of the protein.

19. A method of modulating the expression of a nucleic acid encoding a protein of claim 13, comprising:

- 15 administering an effective amount of an agent which modulates the expression of a nucleic acid encoding the protein.

20. A method of modulating at least one activity of a protein of claim 13, comprising:

- 20 administering an effective amount of an agent which modulates at least one activity of the protein.

21. A method of identifying binding partners for a protein of claim 13, comprising:

exposing said protein to a potential binding partner; and

determining if the potential binding partner binds to said protein, thereby identifying binding partners for the protein.

22. A method of identifying an agent which modulates the interaction between a binding partner of claim 21 and a protein of claim 13, comprising:

5 exposing said protein with said partner to the agent; and

determining whether the agent modulates association of the binding partner with said protein, thereby identifying an agent which modulates association of a binding partner with said protein.

23. A method of modulating the interaction between a binding partner of claim 10 21 and a protein of claim 13, comprising:

administering an effective amount of an agent which modulates association of a binding partner with said protein.

24. A non-human transgenic animal modified to contain a nucleic acid molecule of any of claims 1-4.

15 25. The transgenic animal of claim 24, wherein the nucleic acid molecule contains a mutation that prevents expression of the encoded protein.

26. A method of treating a disease state in a subject, comprising:

20 inserting into a diseased cell a gene construct comprising an isolated nucleic acid molecule of any one of claims 1-4 linked to a promoter or enhancer element such that expression of said nucleic molecule causes suppression of said disease.

27. The method of claim 26, wherein said inserting into a diseased cell is accomplished *in vivo*.

28. The method of claim 26, wherein said inserting into a diseased cell further comprises use of a viral or plasmid agent and is accomplished either *in vitro* or *in vivo*.

29. A method of diagnosing a disease state in a subject, comprising:

determining the level of expression of a nucleic acid molecule or protein of any one of claims 1-4 or 13.

30. The method of claims 26 and 29, wherein the disease state is cancer.

31. The method of claims 26 and 29, wherein the disease state is a malignant neoplasm.

32. The method of claim 31, wherein the malignant neoplasm occurs in the breast, colon, esophagus, kidney, liver, lung, lymph node, ovary, pancreas, prostate, rectum, and/or stomach.

33. A composition comprising a diluent and a polypeptide or protein selected from the group consisting of: an isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising a fragment of at least 10 amino acids of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising conservative amino acid substitutions of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; an isolated polypeptide comprising naturally occurring amino acid sequence variants of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16; and an isolated polypeptide exhibiting at least about 75% amino acid sequence identity with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16.

DRAWINGS

FIG. 1

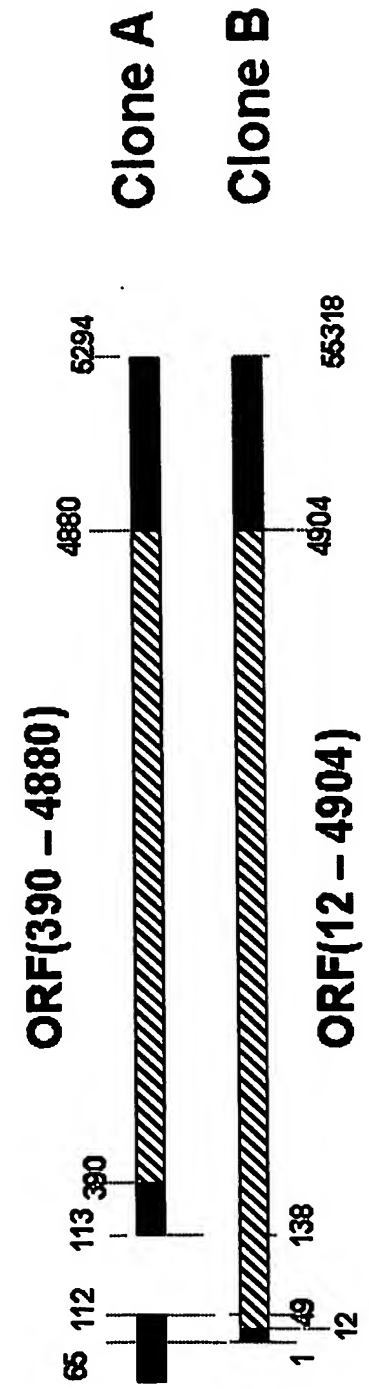


FIG. 2

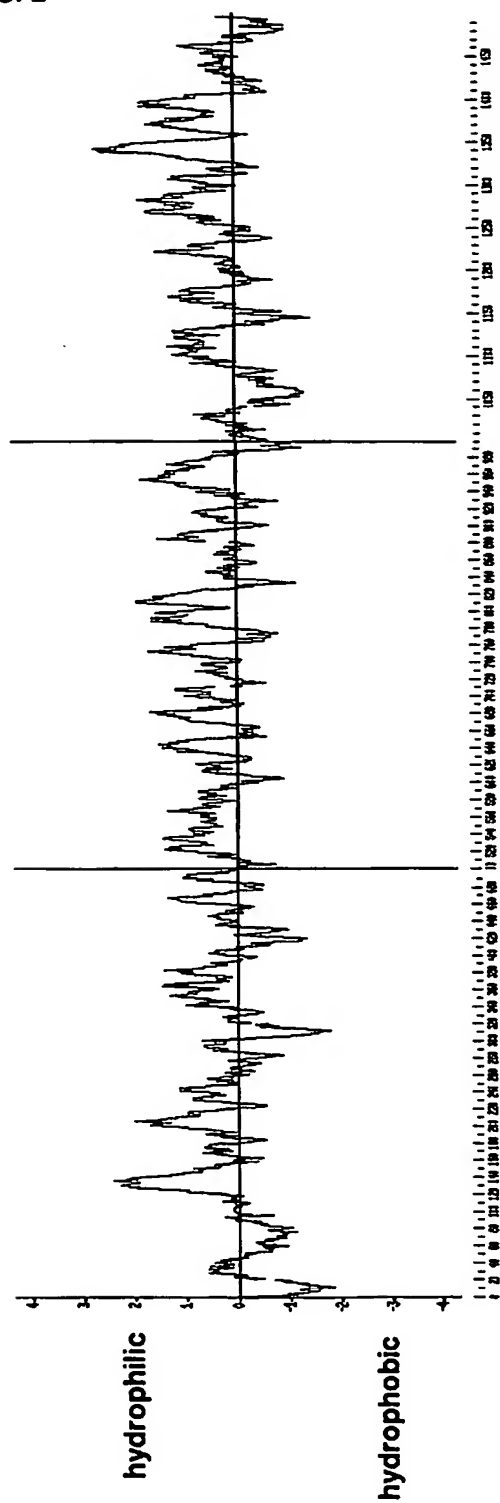


FIG. 3

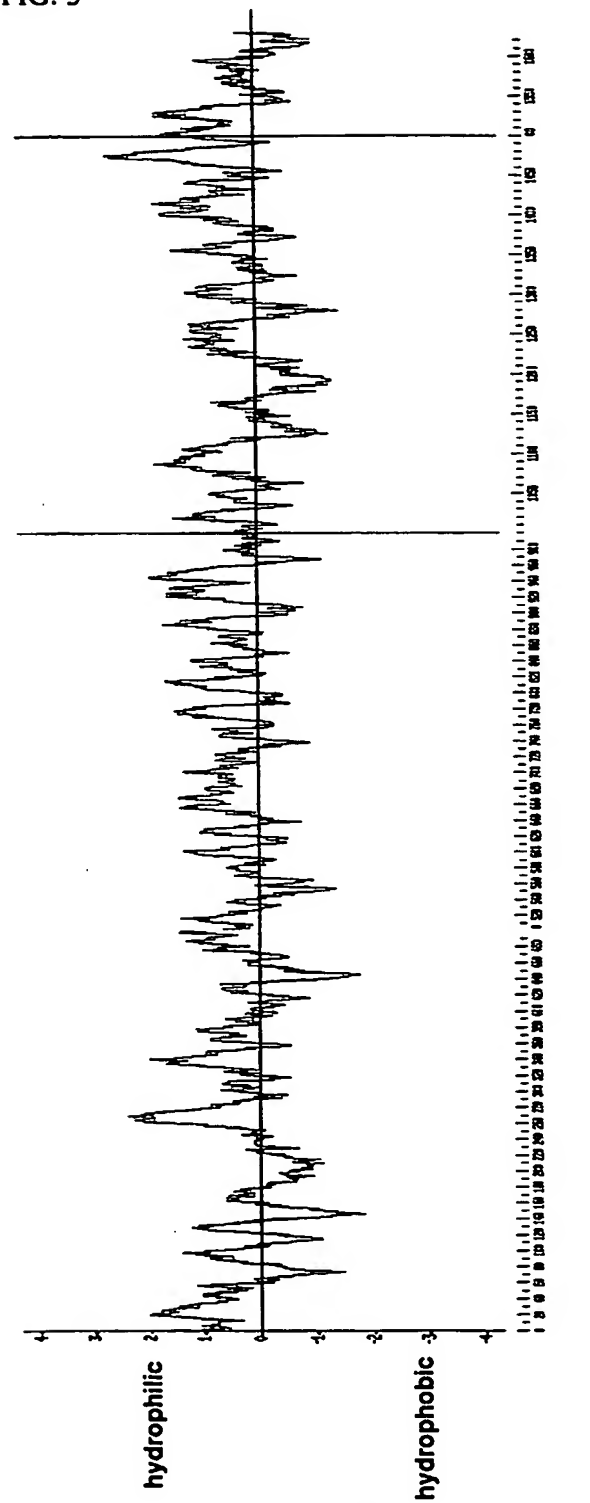


FIG. 4

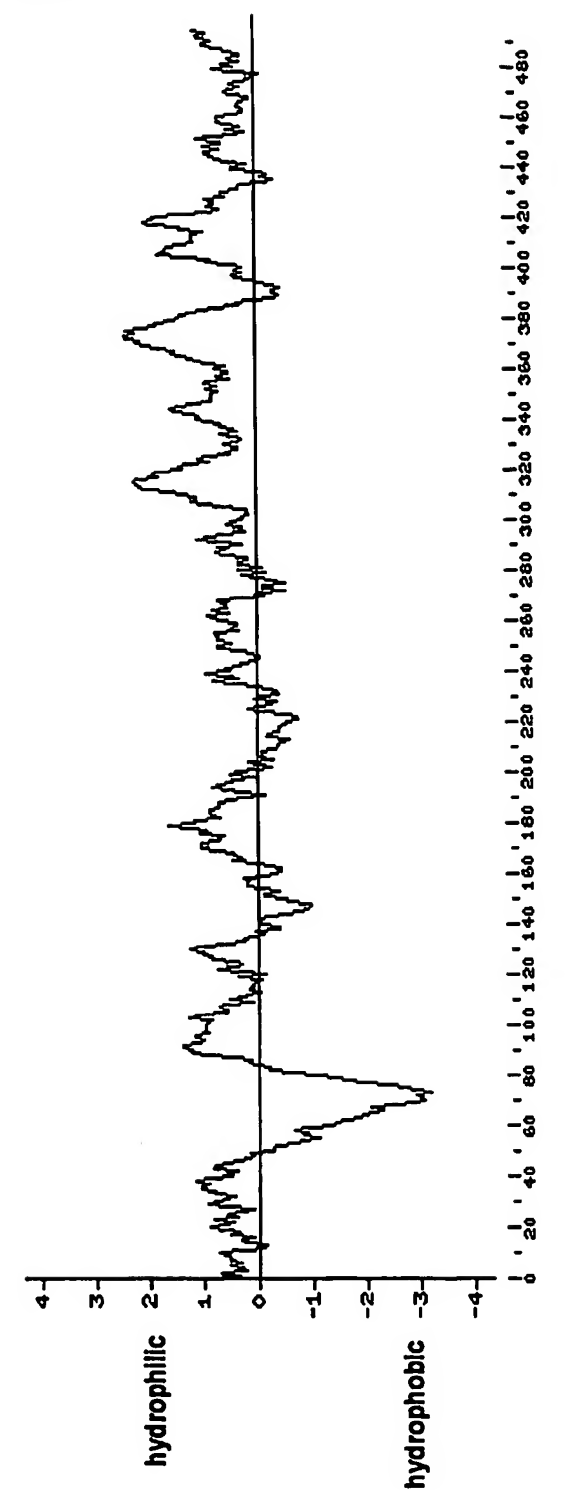


FIG. 5

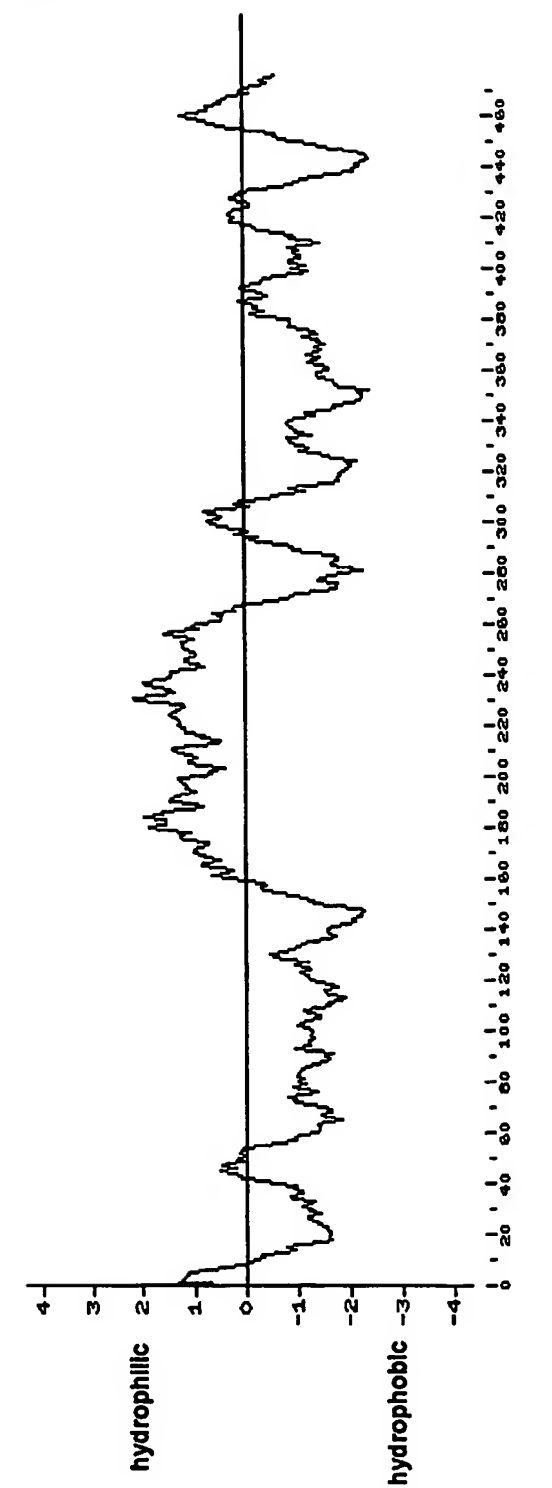


FIG. 6

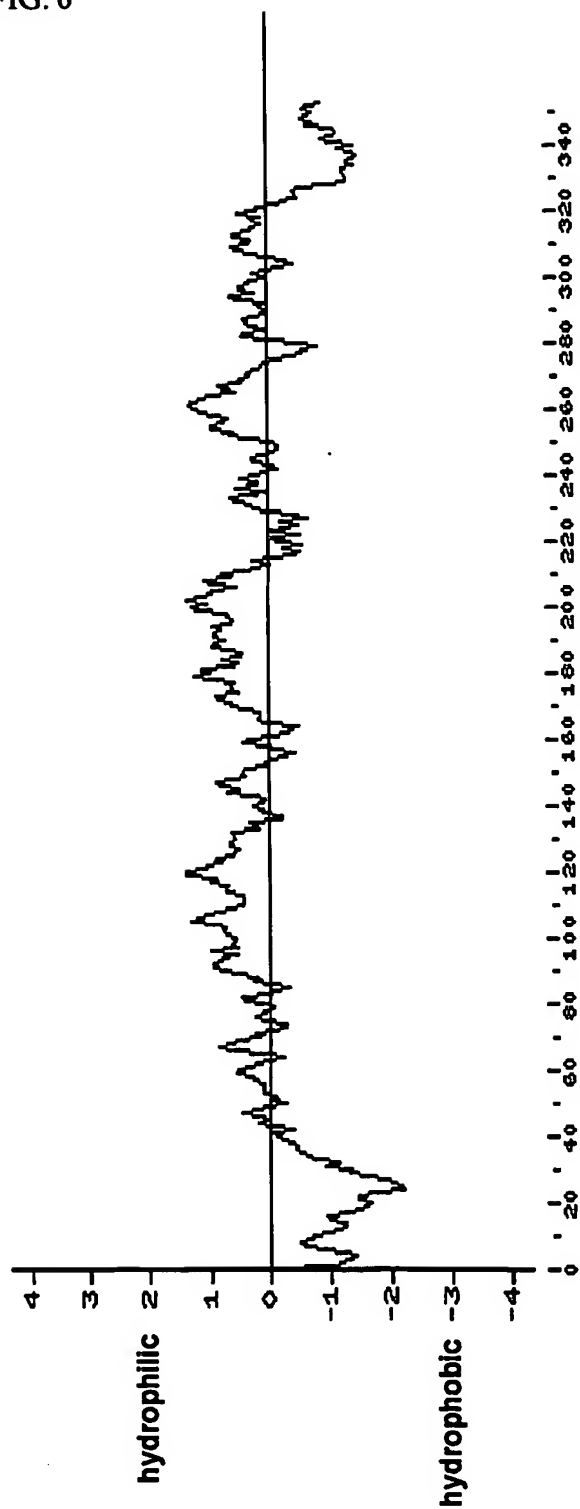


FIG. 7

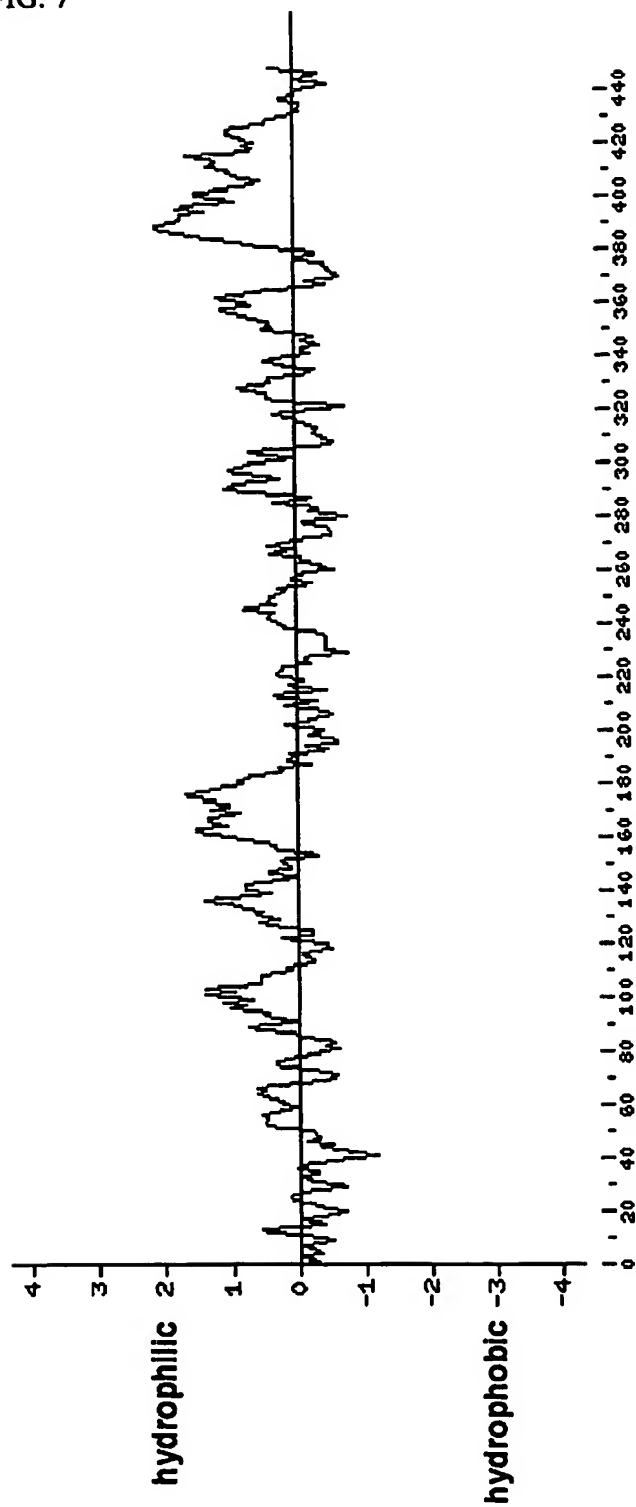


FIG. 8

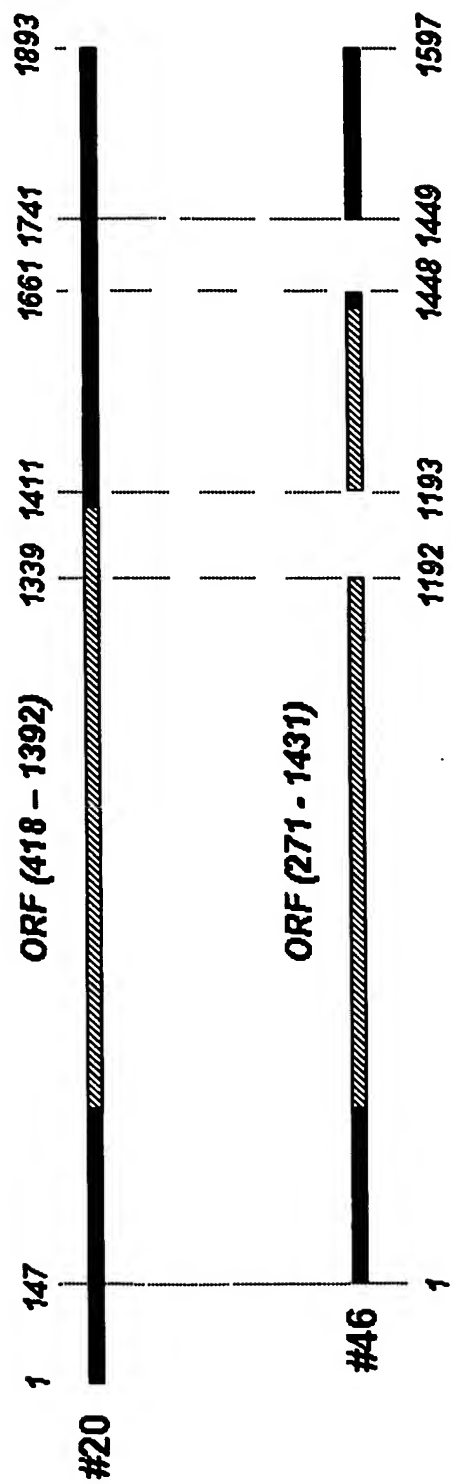


FIG. 9

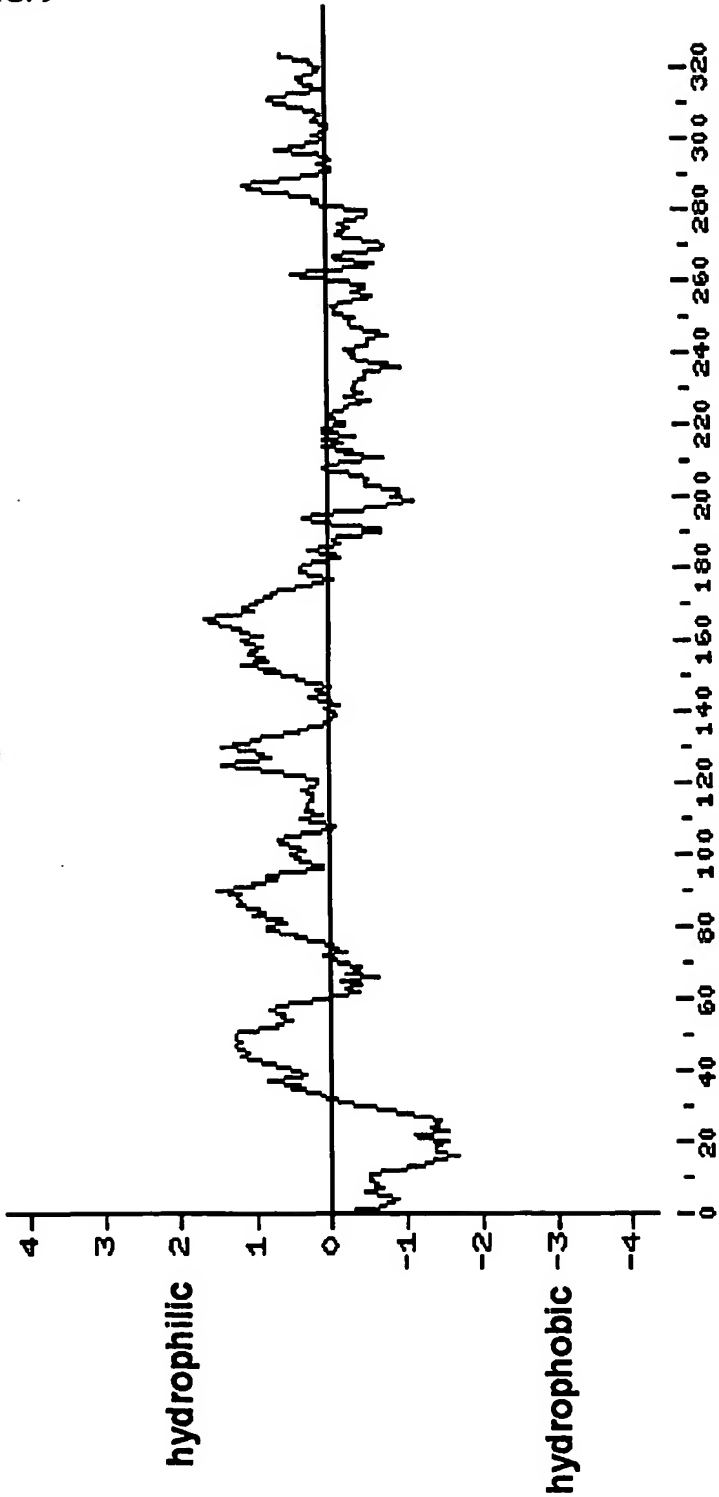
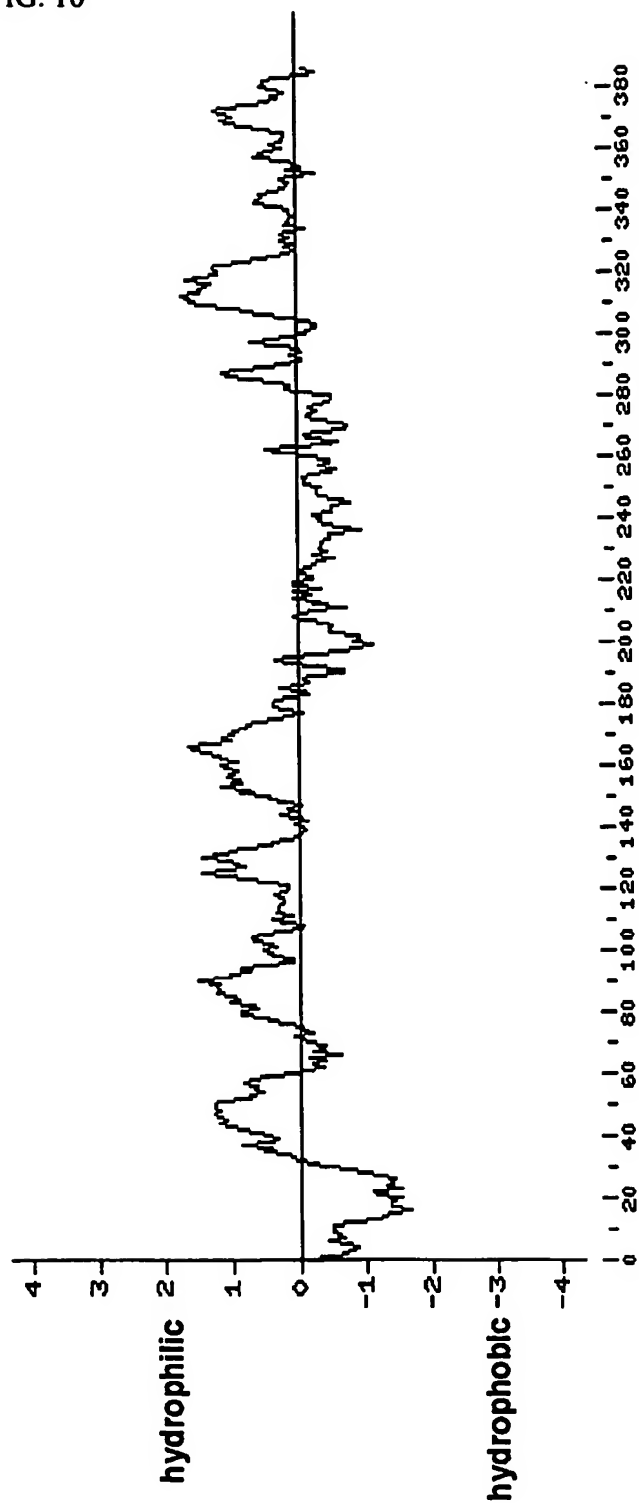


FIG. 10



Sequence Listing

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<120> Gene Families Associated With Cancers

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<151> 2003-01-03

<160> 56

<170> KopatentIn 1.71

<210> 1

<211> 5293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (390) .. (4880)

<223> LBFL109 Clone A

<400> 1

Sequence Listing

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ggaagaagga ggaacatgga gaggagagca gcgggcccag gctgggcagc ctctggatcg	120
aggcctgcct gaaggaggag cttccttccc cgggtggagct ggaggagagc cttcggaatg	180
gagtgctgct ggccaagctg ggccactggt ttgcaccctc cgtgggtccg ttgaagaaga	240
tctacgatgt ggagcagctg cggtagcagg caactggctt acatttccgt cacacagaca	300
acatcaactt ttggctatct gcaatagccc acatcgggtc gccttcgacc ttcttcccag	360
agaccacgga catctatgac aaaaagaac atg ccc cgg gta gtc tac tgc atc	413
Met Pro Arg Val Val Tyr Cys Ile	
1 5	
cat gct ctc agt ctc ttc ctc ttc cgg ctg gga ttg gcc cct cag ata	461
His Ala Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala Pro Gln Ile	
10 15 20	
cat gat cta tac ggg aaa gtg aaa ttc aca gct gag gaa ctc agc aac	509
His Asp Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu Leu Ser Asn	
25 30 35 40	
atg gcg tcc gaa ctg gcc aaa tat ggc ctc cag ctg cct gcc ttc agc	557
Met Ala Ser Glu Leu Ala Lys Tyr Gly Leu Gln Leu Pro Ala Phe Ser	
45 50 55	
aag atc ggg ggc atc ttg gcc aat gag ctc tcg gtg gat gag gct gca	605
Lys Ile Gly Gly Ile Leu Ala Asn Glu Leu Ser Val Asp Glu Ala Ala	
60 65 70	
gtc cat gca gct gtt ctt gcc atc aat gaa gca gtg gag cga ggg gtg	653
Val His Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu Arg Gly Val	
75 80 85	
gtg gag gac acc ctg gct gcc ttg cag aat ccc agt gct ctt ctg gag	701
Val Glu Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala Leu Leu Glu	
90 95 100	

Sequence Listing

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gcc aag atg gag aag gca gcc aat gcc agg aac cat gat gac aga gaa Ala Lys Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp Asp Arg Glu 125 130 135	797
agc cag gac atc tat gac cac tac cta act cag gct gaa atc cag ggc Ser Gln Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu Ile Gln Gly 140 145 150	845
aat atc aac cat gtc aac gtc cat ggg gct cta gaa gtt gtt gat gat Asn Ile Asn His Val Asn Val His Gly Ala Leu Glu Val Val Asp Asp 155 160 165	893
gcc ctg gaa aga cag agc cct gaa gcc ttg ctc aag gcc ctt caa gac Ala Leu Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala Leu Gln Asp 170 175 180	941
cct gcc ctg gcc ctg cga ggg gtg agg aga gac ttt gct gac tgg tac Pro Ala Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala Asp Trp Tyr 185 190 195 200	989
ctg gag cag ctg aac tca gac aga gag cag aag gca cag gag ctg ggc Leu Glu Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln Glu Leu Gly 205 210 215	1037
ctg gtg gag ctt ctg gaa aag gag gaa gtc cag gct ggt gtg gct gca Leu Val Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly Val Ala Ala 220 225 230	1085
gcc aac aca aag ggt gat cag gaa caa gcc atg ctc cac gct gtg cag Ala Asn Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His Ala Val Gln 235 240 245	1133
cgg atc aac aaa gcc atc cgg agg gga gtg gcg gct gac act gtg aag Arg Ile Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp Thr Val Lys 250 255 260	1181

Sequence Listing

gag ctg atg tgc cct gag gcc cag ctg cct cca gtg tac cct gtt gca Glu Leu Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr Pro Val Ala 265 270 275 280	1229
tcg tct atg tac cag ctg gag ctg gca gtg ctc cag cag cag cag ggg Ser Ser Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln Gln Gln Gly 285 290 295	1277
gag ctt ggc cag gag gag ctc ttc gtg gct gtg gag atg ctc tca gct Glu Leu Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met Leu Ser Ala 300 305 310	1325
gtg gtc ctg att aac cgg gcc ctg gag gcc cgg gat gcc agt ggc ttc Val Val Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala Ser Gly Phe 315 320 325	1373
tgg agc agc ctg gtg aac cct gcc aca ggc ctg gct gag gtg gaa gga Trp Ser Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu Val Glu Gly 330 335 340	1421
gaa aat gcc cag cgt tac ttc gat gcc ctg ctg aaa ttg cga cag gag Glu Asn Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu Arg Gln Glu 345 350 355 360	1469
cgt ggg atg ggt gag gac ttc ctg agc tgg aat gac ctg cag gcc acc Arg Gly Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu Gln Ala Thr 365 370 375	1517
gtg agc cag gtc aat gca cag acc cag gaa gag act gac cgg gtc ctt Val Ser Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp Arg Val Leu 380 385 390	1565
gca gtc agc ctc atc aat gag gct ctg gac aaa ggc agc cct gag aag Ala Val Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser Pro Glu Lys 395 400 405	1613
act ctg tct gcc cta ctg ctt cct gca gct ggc cta gat gat gtc agc Thr Leu Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp Asp Val Ser 410 415 420	1661

Sequence Listing

ctc cct gtc gcc cct cgg tac cat ctc ctc ctt gtg gca gcc aaa agg	1709
Leu Pro Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala Ala Lys Arg	
425 430 435 440	
cag aag gcc cag gtg aca ggg gat cct gga gct gtg ctg tgg ctt gag	1757
Gln Lys Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu Trp Leu Glu	
445 450 455	
gag atc cgc cag gga gtg gtc aga gcc aac cag gac act aat aca gct	1805
Glu Ile Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr Asn Thr Ala	
460 465 470	
cag aga atg gct ctt ggt gtg gct gcc atc aat caa gcc atc aag gag	1853
Gln Arg Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala Ile Lys Glu	
475 480 485	
ggc aag gca gcc cag act gag cgg gtg ttg agg aac ccc gca gtg gcc	1901
Gly Lys Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro Ala Val Ala	
490 495 500	
ctt cga ggg gta gtt ccc gac tgt gcc aac ggc tac cag cga gcc ctg	1949
Leu Arg Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln Arg Ala Leu	
505 510 515 520	
gaa agt gcc atg gca aag aaa cag cgt cca gca gac aca gct ttc tgg	1997
Glu Ser Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr Ala Phe Trp	
525 530 535	
ggt caa cat gac atg aag gat ggc act gcc tac tac ttc cat ctg cag	2045
Val Gln His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe His Leu Gln	
540 545 550	
acc ttc cag ggg atc tgg gag caa cct cct ggc tgc ccc ctc aac acc	2093
Thr Phe Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro Leu Asn Thr	
555 560 565	
tct cac ctg acc cgg gag gag atc cag tca gct gtc acc aag gtc act	2141
Ser His Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr Lys Val Thr	
570 575 580	

Sequence Listing

gct gcc tat gac cgc caa cag ctc tgg aaa gcc aac gtc ggc ttt gtt Ala Ala Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val Gly Phe Val	2189
585 590 595 600	
atc cag ctc cag gcc cgc ctc cgt ggc ttc cta gtt cgg cag aag ttt Ile Gln Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg Gln Lys Phe	2237
605 610 615	
gct gag cat tcc cac ttt ctg agg acc tgg ctc cca gca gtc atc aag Ala Glu His Ser His Phe Leu Arg Thr Trp Leu Pro Ala Val Ile Lys	2285
620 625 630	
atc cag gct cat tgg cgg ggt tat agg cag cgg aag att tac ctg gag Ile Gln Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile Tyr Leu Glu	2333
635 640 645	
tgg ttg cag tat ttt aaa gca aac ctg gat gcc ata atc aag atc cag Trp Leu Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile Lys Ile Gln	2381
650 655 660	
gcc tgg gcc cgg atg tgg gca gct cgg agg caa tac ctg agg cgt ctg Ala Trp Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu Arg Arg Leu	2429
665 670 675 680	
cac tac ttc cag aag aat gtt aac tcc att gtg aag atc cag gca ttt His Tyr Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile Gln Ala Phe	2477
685 690 695	
ttc cga gcc agg aaa gcc caa gat gac tac agg ata tta gtg cat gca Phe Arg Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu Val His Ala	2525
700 705 710	
ccc cac cct cct ctc agt gtg gta cgc aga ttt gcc cat ctc ttg aat Pro His Pro Pro Leu Ser Val Val Arg Arg Phe Ala His Leu Leu Asn	2573
715 720 725	
caa agc cag caa gac ttc ttg gct gag gca gag ctg ctg aag ctc cag Gln Ser Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu Lys Leu Gln	2621
730 735 740	

Sequence Listing

gaa gag gta gtt agg aag atc cga tcc aat cag cag ctg gag cag gac Glu Glu Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu Glu Gln Asp 745 750 755 760	2669
ctc aac atc atg gac atc aag att ggc ctg ctg gtg aag aac cgg atc Leu Asn Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Arg Ile 765 770 775	2717
act ctg cag gaa gtg gtc tcc cac tgc aag aag ctg acc aag agg aat Thr Leu Gln Glu Val Val Ser His Cys Lys Lys Leu Thr Lys Arg Asn 780 785 790	2765
aag gaa cag ctg tca gat atg atg gtt ctg gac aag cag aag ggt tta Lys Glu Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln Lys Gly Leu 795 800 805	2813
aag tcg ctg agc aaa gag aaa cgg cag aaa cta gaa gca tac caa cac Lys Ser Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala Tyr Gln His 810 815 820	2861
ctc ttc tac ctg ctc cag act cag ccc atc tac ctg gcc aag ctg atc Leu Phe Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala Lys Leu Ile 825 830 835 840	2909
ttt cag atg cca cag aac aaa acc acc aag ttc atg gag gca gtg att Phe Gln Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu Ala Val Ile 845 850 855	2957
ttc agc ctg tac aac tat gcc tcc agc cgc cga gag gcc tat ctc ctg Phe Ser Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala Tyr Leu Leu 860 865 870	3005
ctc cag ctg ttc aag aca gca ctc cag gag gaa atc aag tca aag gtg Leu Gln Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val 875 880 885	3053
gag cag ccc cag gac gtg gtg aca ggc aac cca aca gtg gtg agg ctg Glu Gln Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val Val Arg Leu 890 895 900	3101

Sequence Listing

gtg gtg aga ttc tac cgt aat ggg cgg gga cag agt gcc ctg cag gag Val Val Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala Leu Gln Glu 905 910 915 920	3149
att ctg ggc aag gtt atc cag gat gtg cta gaa gac aaa gtg ctc agc Ile Leu Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys Val Leu Ser 925 930 935	3197
gtc cac aca gac cct gtc cac ctc tat aag aac tgg atc aac cag act Val His Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile Asn Gln Thr 940 945 950	3245
gag gcc cag aca ggg cag cgc agc cat ctc cca tat gat gtc acc ccg Glu Ala Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp Val Thr Pro 955 960 965	3293
gag cag gcc ttg agc cac ccc gag gtc cag aga cga ctg gac atc gcc Glu Gln Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu Asp Ile Ala 970 975 980	3341
cta cgc aac ctc ctc gcc atg act gat aag ttc ctt tta gcc atc acc Leu Arg Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu Ala Ile Thr 985 990 995 1000	3389
tca tct gtg gac caa att ccg tat ggg atg cga tat gtg gcc aaa gtc Ser Ser Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val Ala Lys Val 1005 1010 1015	3437
ctg aag gca act ctg gca gag aaa ttc cct gac gcc aca gac agc gag Leu Lys Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr Asp Ser Glu 1020 1025 1030	3485
gtc tat aag gtg gtc ggg aac ctc ctg tac tac cgc ttc ctg aac cca Val Tyr Lys Val Val Gly Asn Leu Leu Tyr Tyr Arg Phe Leu Asn Pro 1035 1040 1045	3533
gct gtg gtg gct cct gac gcc ttc gac att gtg gcc atg gca gct ggt Ala Val Val Ala Pro Asp Ala Phe Asp Ile Val Ala Met Ala Ala Gly 1050 1055 1060	3581

Sequence Listing

gga gcc ctg gct gcc ccc cag cgc cat gcc ctg ggg gct gtg gct cag Gly Ala Leu Ala Ala Pro Gln Arg His Ala Leu Gly Ala Val Ala Gln 1065 1070 1075 1080	3629
ctc cta cag cac gct gcg gct ggc aag gcc ttc tct ggg cag agc cag Leu Leu Gln His Ala Ala Ala Gly Lys Ala Phe Ser Gly Gln Ser Gln 1085 1090 1095	3677
cac cta cgg gtc ctg aat gac tat ctg gag gaa aca cac ctc aag ttc His Leu Arg Val Leu Asn Asp Tyr Leu Glu Glu Thr His Leu Lys Phe 1100 1105 1110	3725
agg aag ttc atc cat aga gcc tgc cag gtg cca gag cca gag gag cgt Arg Lys Phe Ile His Arg Ala Cys Gln Val Pro Glu Pro Glu Glu Arg 1115 1120 1125	3773
ttt gca gtg gac gag tac tca gac atg gtg gct gtg gcc aaa ccc atg Phe Ala Val Asp Glu Tyr Ser Asp Met Val Ala Val Ala Lys Pro Met 1130 1135 1140	3821
gtg tac atc acc gtg ggg gag ctg gtc aac acg cac agg ctg ttg ctg Val Tyr Ile Thr Val Gly Glu Leu Val Asn Thr His Arg Leu Leu Leu 1145 1150 1155 1160	3869
gag cac cag gac tgc att gcc cct gat cac caa gac ccc ctg cat gag Glu His Gln Asp Cys Ile Ala Pro Asp His Gln Asp Pro Leu His Glu 1165 1170 1175	3917
ctc ctg gag gat ctt ggg gag ctg ccc acc atc cct gac ctt att ggt Leu Leu Glu Asp Leu Gly Glu Leu Pro Thr Ile Pro Asp Leu Ile Gly 1180 1185 1190	3965
gag agc atc gct gca gat ggg cac aca gac ctg agc aag cta gaa gtg Glu Ser Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys Leu Glu Val 1195 1200 1205	4013
tcc ctg acg ctg acc aac aag ttt gaa gga cta gag gca gat gct gat Ser Leu Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala Asp Ala Asp 1210 1215 1220	4061

Sequence Listing

gac tcc aac acc cgt agc ctg ctt ctg agc acc aag cag ctg ttg gcc	4109
Asp Ser Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln Leu Leu Ala	
1225 1230 1235 1240	
gat atc ata cag ttc cat cct ggg gac acc ctc aag gag atc ctg tcc	4157
Asp Ile Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu Ile Leu Ser	
1245 1250 1255	
ctc tcg gct tcc aga gag caa gaa gca gcc cac aag cag ctg atg agc	4205
Leu Ser Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln Leu Met Ser	
1260 1265 1270	
cga cgc cag gcc tgt aca gcc cag aca ccg gag cca ctg cga cga cac	4253
Arg Arg Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu Arg Arg His	
1275 1280 1285	
cgc tca ctg aca gct cac tcc ctc ctg cca ctg gca gag aag cag cgg	4301
Arg Ser Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu Lys Gln Arg	
1290 1295 1300	
cgc gtc ctg cgg aac ctg cgc cga ctt gaa gcc ctg ggg ttg gtc agc	4349
Arg Val Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly Leu Val Ser	
1305 1310 1315 1320	
gcc aga aat ggc tac cag ggg cta gtg gac gag ctg gcc aag gac atc	4397
Ala Arg Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala Lys Asp Ile	
1325 1330 1335	
cgc aac cag cac aga cac agg cac agg cgg aag gca gag ctg gtg aag	4445
Arg Asn Gln His Arg His Arg His Arg Arg Lys Ala Glu Leu Val Lys	
1340 1345 1350	
ctg cag gcc aca tta cag ggc ctg agc act aag acc acc ttc tat gag	4493
Leu Gln Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr Phe Tyr Glu	
1355 1360 1365	
gag cag ggt gac tac tac agc cag tac atc cgg gcc tgc ctg gac cac	4541
Glu Gln Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys Leu Asp His	
1370 1375 1380	

Sequence Listing

ctg gcc ccc gac tcc aag agt tct ggg aag ggg aag aag cag cct tct	4589
Leu Ala Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys Gln Pro Ser	
1385 1390 1395 1400	
ctt cat tac act gct gct cag ctc ctg gaa aag ggt gtc ttg gtg gaa	4637
Leu His Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val Leu Val Glu	
1405 1410 1415	
att gaa gat ctt ccc gcc tct cac ttc aga aac gtc atc ttt gac atc	4685
Ile Glu Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile Phe Asp Ile	
1420 1425 1430	
acg ccg gga gat gag gca gga aag ttt gaa gta aat gcc aag ttc ctg	4733
Thr Pro Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala Lys Phe Leu	
1435 1440 1445	
ggt gtg gac atg gag cga ttt cag ctt cac tat cag gat ctc ctg cag	4781
Gly Val Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp Leu Leu Gln	
1450 1455 1460	
ctc cag tat gag ggt gtg gct gtc atg aaa ctc ttc aac aag gcc aaa	4829
Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn Lys Ala Lys	
1465 1470 1475 1480	
gtc aat gtc aac ctt ctc atc ttc ctc ctc aac aag aag ttt ttg cgg	4877
Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys Phe Leu Arg	
1485 1490 1495	
aag tgacagaggc aaaggggtgct acccaagccc ctcttacctc tctggatgct	4930
Lys	
ttctttaaca ctaactcacc actgtgcttc cctgcagaca ccagagctc aggactgggc	4990
aaggccagg gattctcacc ccttccccag ctgggaggag cttgcctgcc tggccacaga	5050
cagtgtatct tctaattggc taaagtgggc cttgcccaga gtccagctgt gtggctttta	5110
tcatgcatga caaacccctg gctttcctgc cagatggatt ctcacccctt acagctgact	5170
cttcaggca atttccatag atctgcagtc ctgcctctgc cacagtctct ctgttgctcc	5230

Sequence Listing

cacatctacc caacttcctg tactgttgcc ctctgatgt taataaaagc agctgttact 5290

ccc 5293

<210> 2

<211> 1497

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Arg Val Val Tyr Cys Ile His Ala Leu Ser Leu Phe Leu Phe
1 5 10 15

Arg Leu Gly Leu Ala Pro Gln Ile His Asp Leu Tyr Gly Lys Val Lys
20 25 30

Phe Thr Ala Glu Glu Leu Ser Asn Met Ala Ser Glu Leu Ala Lys Tyr
35 40 45

Gly Leu Gln Leu Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn
50 55 60

Glu Leu Ser Val Asp Glu Ala Ala Val His Ala Ala Val Leu Ala Ile
65 70 75 80

Asn Glu Ala Val Glu Arg Gly Val Val Glu Asp Thr Leu Ala Ala Leu
85 90 95

Gln Asn Pro Ser Ala Leu Leu Glu Asn Leu Arg Glu Pro Leu Ala Ala
100 105 110

Val Tyr Gln Glu Met Leu Ala Gln Ala Lys Met Glu Lys Ala Ala Asn
115 120 125

Ala Arg Asn His Asp Asp Arg Glu Ser Gln Asp Ile Tyr Asp His Tyr
130 135 140

Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn His Val Asn Val His

Sequence Listing

145	150	155	160
Gly Ala Leu Glu Val Val Asp Asp Ala Leu Glu Arg Gln Ser Pro Glu			
165	170	175	
Ala Leu Leu Lys Ala Leu Gln Asp Pro Ala Leu Ala Leu Arg Gly Val			
180	185	190	
Arg Arg Asp Phe Ala Asp Trp Tyr Leu Glu Gln Leu Asn Ser Asp Arg			
195	200	205	
Glu Gln Lys Ala Gln Glu Leu Gly Leu Val Glu Leu Leu Glu Lys Glu			
210	215	220	
Glu Val Gln Ala Gly Val Ala Ala Ala Asn Thr Lys Gly Asp Gln Glu			
225	230	235	240
Gln Ala Met Leu His Ala Val Gln Arg Ile Asn Lys Ala Ile Arg Arg			
245	250	255	
Gly Val Ala Ala Asp Thr Val Lys Glu Leu Met Cys Pro Glu Ala Gln			
260	265	270	
Leu Pro Pro Val Tyr Pro Val Ala Ser Ser Met Tyr Gln Leu Glu Leu			
275	280	285	
Ala Val Leu Gln Gln Gln Gln Gly Glu Leu Gly Gln Glu Glu Leu Phe			
290	295	300	
Val Ala Val Glu Met Leu Ser Ala Val Val Leu Ile Asn Arg Ala Leu			
305	310	315	320
Glu Ala Arg Asp Ala Ser Gly Phe Trp Ser Ser Leu Val Asn Pro Ala			
325	330	335	
Thr Gly Leu Ala Glu Val Glu Gly Glu Asn Ala Gln Arg Tyr Phe Asp			
340	345	350	
Ala Leu Leu Lys Leu Arg Gln Glu Arg Gly Met Gly Glu Asp Phe Leu			
355	360	365	

Sequence Listing

Ser Trp Asn Asp Leu Gln Ala Thr Val Ser Gln Val Asn Ala Gln Thr
370 375 380

Gln Glu Glu Thr Asp Arg Val Leu Ala Val Ser Leu Ile Asn Glu Ala
385 390 395 400

Leu Asp Lys Gly Ser Pro Glu Lys Thr Leu Ser Ala Leu Leu Leu Pro
405 410 415

Ala Ala Gly Leu Asp Asp Val Ser Leu Pro Val Ala Pro Arg Tyr His
420 425 430

Leu Leu Leu Val Ala Ala Lys Arg Gln Lys Ala Gln Val Thr Gly Asp
435 440 445

Pro Gly Ala Val Leu Trp Leu Glu Glu Ile Arg Gln Gly Val Val Arg
450 455 460

Ala Asn Gln Asp Thr Asn Thr Ala Gln Arg Met Ala Leu Gly Val Ala
465 470 475 480

Ala Ile Asn Gln Ala Ile Lys Glu Gly Lys Ala Ala Gln Thr Glu Arg
485 490 495

Val Leu Arg Asn Pro Ala Val Ala Leu Arg Gly Val Val Pro Asp Cys
500 505 510

Ala Asn Gly Tyr Gln Arg Ala Leu Glu Ser Ala Met Ala Lys Lys Gln
515 520 525

Arg Pro Ala Asp Thr Ala Phe Trp Val Gln His Asp Met Lys Asp Gly
530 535 540

Thr Ala Tyr Tyr Phe His Leu Gln Thr Phe Gln Gly Ile Trp Glu Gln
545 550 555 560

Pro Pro Gly Cys Pro Leu Asn Thr Ser His Leu Thr Arg Glu Glu Ile
565 570 575

Sequence Listing

Gln Ser Ala Val Thr Lys Val Thr Ala Ala Tyr Asp Arg Gln Gln Leu
 580 585 590

Trp Lys Ala Asn Val Gly Phe Val Ile Gln Leu Gln Ala Arg Leu Arg
 595 600 605

Gly Phe Leu Val Arg Gln Lys Phe Ala Glu His Ser His Phe Leu Arg
 610 615 620

Thr Trp Leu Pro Ala Val Ile Lys Ile Gln Ala His Trp Arg Gly Tyr
 625 630 635 640

Arg Gln Arg Lys Ile Tyr Leu Glu Trp Leu Gln Tyr Phe Lys Ala Asn
 645 650 655

Leu Asp Ala Ile Ile Lys Ile Gln Ala Trp Ala Arg Met Trp Ala Ala
 660 665 670

Arg Arg Gln Tyr Leu Arg Arg Leu His Tyr Phe Gln Lys Asn Val Asn
 675 680 685

Ser Ile Val Lys Ile Gln Ala Phe Phe Arg Ala Arg Lys Ala Gln Asp
 690 695 700

Asp Tyr Arg Ile Leu Val His Ala Pro His Pro Pro Leu Ser Val Val
 705 710 715 720

Arg Arg Phe Ala His Leu Leu Asn Gln Ser Gln Gln Asp Phe Leu Ala
 725 730 735

Glu Ala Glu Leu Leu Lys Leu Gln Glu Glu Val Val Arg Lys Ile Arg
 740 745 750

Ser Asn Gln Gln Leu Glu Gln Asp Leu Asn Ile Met Asp Ile Lys Ile
 755 760 765

Gly Leu Leu Val Lys Asn Arg Ile Thr Leu Gln Glu Val Val Ser His
 770 775 780

Cys Lys Lys Leu Thr Lys Arg Asn Lys Glu Gln Leu Ser Asp Met Met

Sequence Listing

785	790	795	800
Val Leu Asp Lys Gln Lys Gly Leu Lys Ser Leu Ser Lys Glu Lys Arg			
805	810	815	
Gln Lys Leu Glu Ala Tyr Gln His Leu Phe Tyr Leu Leu Gln Thr Gln			
820	825	830	
Pro Ile Tyr Leu Ala Lys Leu Ile Phe Gln Met Pro Gln Asn Lys Thr			
835	840	845	
Thr Lys Phe Met Glu Ala Val Ile Phe Ser Leu Tyr Asn Tyr Ala Ser			
850	855	860	
Ser Arg Arg Glu Ala Tyr Leu Leu Leu Gln Leu Phe Lys Thr Ala Leu			
865	870	875	880
Gln Glu Glu Ile Lys Ser Lys Val Glu Gln Pro Gln Asp Val Val Thr			
885	890	895	
Gly Asn Pro Thr Val Val Arg Leu Val Val Arg Phe Tyr Arg Asn Gly			
900	905	910	
Arg Gly Gln Ser Ala Leu Gln Glu Ile Leu Gly Lys Val Ile Gln Asp			
915	920	925	
Val Leu Glu Asp Lys Val Leu Ser Val His Thr Asp Pro Val His Leu			
930	935	940	
Tyr Lys Asn Trp Ile Asn Gln Thr Glu Ala Gln Thr Gly Gln Arg Ser			
945	950	955	960
His Leu Pro Tyr Asp Val Thr Pro Glu Gln Ala Leu Ser His Pro Glu			
965	970	975	
Val Gln Arg Arg Leu Asp Ile Ala Leu Arg Asn Leu Leu Ala Met Thr			
980	985	990	
Asp Lys Phe Leu Leu Ala Ile Thr Ser Ser Val Asp Gln Ile Pro Tyr			
995	1000	1005	

Sequence Listing

Gly Met Arg Tyr Val Ala Lys Val Leu Lys Ala Thr Leu Ala Glu Lys
1010 1015 1020

Phe Pro Asp Ala Thr Asp Ser Glu Val Tyr Lys Val Val Gly Asn Leu
1025 1030 1035 1040

Leu Tyr Tyr Arg Phe Leu Asn Pro Ala Val Val Ala Pro Asp Ala Phe
1045 1050 1055

Asp Ile Val Ala Met Ala Ala Gly Gly Ala Leu Ala Ala Pro Gln Arg
1060 1065 1070

His Ala Leu Gly Ala Val Ala Gln Leu Leu Gln His Ala Ala Ala Gly
1075 1080 1085

Lys Ala Phe Ser Gly Gln Ser Gln His Leu Arg Val Leu Asn Asp Tyr
1090 1095 1100

Leu Glu Glu Thr His Leu Lys Phe Arg Lys Phe Ile His Arg Ala Cys
1105 1110 1115 1120

Gln Val Pro Glu Pro Glu Glu Arg Phe Ala Val Asp Glu Tyr Ser Asp
1125 1130 1135

Met Val Ala Val Ala Lys Pro Met Val Tyr Ile Thr Val Gly Glu Leu
1140 1145 1150

Val Asn Thr His Arg Leu Leu Leu Glu His Gln Asp Cys Ile Ala Pro
1155 1160 1165

Asp His Gln Asp Pro Leu His Glu Leu Leu Glu Asp Leu Gly Glu Leu
1170 1175 1180

Pro Thr Ile Pro Asp Leu Ile Gly Glu Ser Ile Ala Ala Asp Gly His
1185 1190 1195 1200

Thr Asp Leu Ser Lys Leu Glu Val Ser Leu Thr Leu Thr Asn Lys Phe
1205 1210 1215

Sequence Listing

Glu Gly Leu Glu Ala Asp Ala Asp Asp Ser Asn Thr Arg Ser Leu Leu
1220 1225 1230

Leu Ser Thr Lys Gln Leu Leu Ala Asp Ile Ile Gln Phe His Pro Gly
1235 1240 1245

Asp Thr Leu Lys Glu Ile Leu Ser Leu Ser Ala Ser Arg Glu Gln Glu
1250 1255 1260

Ala Ala His Lys Gln Leu Met Ser Arg Arg Gln Ala Cys Thr Ala Gln
1265 1270 1275 1280

Thr Pro Glu Pro Leu Arg Arg His Arg Ser Leu Thr Ala His Ser Leu
1285 1290 1295

Leu Pro Leu Ala Glu Lys Gln Arg Arg Val Leu Arg Asn Leu Arg Arg
1300 1305 1310

Leu Glu Ala Leu Gly Leu Val Ser Ala Arg Asn Gly Tyr Gln Gly Leu
1315 1320 1325

Val Asp Glu Leu Ala Lys Asp Ile Arg Asn Gln His Arg His Arg His
1330 1335 1340

Arg Arg Lys Ala Glu Leu Val Lys Leu Gln Ala Thr Leu Gln Gly Leu
1345 1350 1355 1360

Ser Thr Lys Thr Thr Phe Tyr Glu Glu Gln Gly Asp Tyr Tyr Ser Gln
1365 1370 1375

Tyr Ile Arg Ala Cys Leu Asp His Leu Ala Pro Asp Ser Lys Ser Ser
1380 1385 1390

Gly Lys Gly Lys Lys Gln Pro Ser Leu His Tyr Thr Ala Ala Gln Leu
1395 1400 1405

Leu Glu Lys Gly Val Leu Val Glu Ile Glu Asp Leu Pro Ala Ser His
1410 1415 1420

Phe Arg Asn Val Ile Phe Asp Ile Thr Pro Gly Asp Glu Ala Gly Lys

Sequence Listing

1425 1430 1435 1440

Phe Glu Val Asn Ala Lys Phe Leu Gly Val Asp Met Glu Arg Phe Gln

1445

1450

1455

Leu His Tyr Gln Asp Leu Leu Gln Leu Gln Tyr Glu Gly Val Ala Val

1460

1465

1470

Met Lys Leu Phe Asn Lys Ala Lys Val Asn Val Asn Leu Leu Ile Phe

1475

1480

1485

Leu Leu Asn Lys Lys Phe Leu Arg Lys

1490

1495

<210> 3

<211> 5317

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)..(4904)

<223> LBFL109 Clone B

<400> 3

gaaggaggaa c atg gag agg aga gca gcg ggc cca ggc tgg gca 44

Met Glu Arg Arg Ala Ala Gly Pro Gly Trp Ala

1

5

10

gcc tat gaa cgc ctc aca gct gag gag atg gat gag cag agg cgg cag 92

Ala Tyr Glu Arg Leu Thr Ala Glu Glu Met Asp Glu Gln Arg Arg Gln

15

20

25

aat gtt gcc tat cag tac ctg tgc cgg ctg gag gag gcc aag cgc tgg 140

Asn Val Ala Tyr Gln Tyr Leu Cys Arg Leu Glu Glu Ala Lys Arg Trp

30

35

40

atg gag gcc tgc ctg aag gag gag ctt cct tcc ccg gtg gag ctg gag 188

Sequence Listing

Met	Glu	Ala	Cys	Leu	Lys	Glu	Glu	Leu	Pro	Ser	Pro	Val	Glu	Leu	Glu		
45						50					55						
gag agc ctt cgg aat gga gtg ctg ctg gcc aag ctg ggc cac tgt ttt																	236
Glu Ser Leu Arg Asn Gly Val Leu Leu Ala Lys Leu Gly His Cys Phe																	
60					65				70						75		
gca ccc tcc gtg gtt ccg ttg aag aag atc tac gat gtg gag cag ctg																	284
Ala Pro Ser Val Val Pro Leu Lys Lys Ile Tyr Asp Val Glu Gln Leu																	
				80				85						90			
cgg tac cag gca act ggc tta cat ttc cgt cac aca gac aac atc aac																	332
Arg Tyr Gln Ala Thr Gly Leu His Phe Arg His Thr Asp Asn Ile Asn																	
			95				100						105				
ttt tgg cta tct gca ata gcc cac atc ggt ctg cct tcg acc ttc ttc																	380
Phe Trp Leu Ser Ala Ile Ala His Ile Gly Leu Pro Ser Thr Phe Phe																	
		110				115					120						
cca gag acc acg gac atc tat gac aaa aag aac atg ccc cgg gta gtc																	428
Pro Glu Thr Thr Asp Ile Tyr Asp Lys Lys Asn Met Pro Arg Val Val																	
		125				130					135						
tac tgc atc cat gct ctc agt ctc ttc ctc ttc cgg ctg gga ttg gcc																	476
Tyr Cys Ile His Ala Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala																	
140					145				150					155			
cct cag ata cat gat cta tac ggg aaa gtg aaa ttc aca gct gag gaa																	524
Pro Gln Ile His Asp Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu																	
				160				165						170			
ctc agc aac atg gcg tcc gaa ctg gcc aaa tat ggc ctc cag ctg cct																	572
Leu Ser Asn Met Ala Ser Glu Leu Ala Lys Tyr Gly Leu Gln Leu Pro																	
			175				180						185				
gcc ttc agc aag atc ggg ggc atc ttg gcc aat gag ctc tcg gtg gat																	620
Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn Glu Leu Ser Val Asp																	
			190				195						200				
gaq gct gca gtc cat gca gct gtt ctt gcc atc aat gaa gca gtg gag																	668

Sequence Listing

Glu Ala Ala Val His Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu	
205	210 215
cga ggg gtg gtg gag gac acc ctg gct gcc ttg cag aat ccc agt gct	716
Arg Gly Val Val Glu Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala	
220	225 230 235
ctt ctg gag aat ctc cga gag cct ctg gca gcc gtc tac cag gag atg	764
Leu Leu Glu Asn Leu Arg Glu Pro Leu Ala Ala Val Tyr Gln Glu Met	
240	245 250
ctg gcc cag gcc aag atg gag aag gca gcc aat gcc agg aac cat gat	812
Leu Ala Gln Ala Lys Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp	
255	260 265
gac aga gaa agc cag gac atc tat gac cac tac cta act cag gct gaa	860
Asp Arg Glu Ser Gln Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu	
270	275 280
atc cag ggc aat atc aac cat gtc aac gtc cat ggg gct cta gaa gtt	908
Ile Gln Gly Asn Ile Asn His Val Asn Val His Gly Ala Leu Glu Val	
285	290 295
gtt gat gat gcc ctg gaa aga cag agc cct gaa gcc ttg ctc aag gcc	956
Val Asp Asp Ala Leu Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala	
300	305 310 315
ctt caa gac cct gcc ctg gcc ctg cga ggg gtg agg aga gac ttt gct	1004
Leu Gln Asp Pro Ala Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala	
320	325 330
gac tgg tac ctg gag cag ctg aac tca gac aga gag cag aag gca cag	1052
Asp Trp Tyr Leu Glu Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln	
335	340 345
gag ctg ggc ctg gtg gag ctt ctg gaa aag gag gaa gtc cag gct ggt	1100
Glu Leu Gly Leu Val Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly	
350	355 360
gtg gct gca gcc aac aca aag ggt gat cag gaa caa gcc atg ctc cac	1148

Sequence Listing

Val Ala Ala Ala Asn Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His	
365	370 375
gct gtg cag cgg atc aac aaa gcc atc cgg agg gga gtg gcg gct gac	1196
Ala Val Gln Arg Ile Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp	
380	385 390 395
act gtg aag gag ctg atg tgc cct gag gcc cag ctg cct cca gtg tac	1244
Thr Val Lys Glu Leu Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr	
400	405 410
cct gtt gca tcg tct atg tac cag ctg gag ctg gca gtg ctc cag cag	1292
Pro Val Ala Ser Ser Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln	
415	420 425
cag cag ggg gag ctt ggc cag gag gag ctc ttc gtg gct gtg gag atg	1340
Gln Gln Gly Glu Leu Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met	
430	435 440
ctc tca gct gtg gtc ctg att aac cgg gcc ctg gag gcc cgg gat gcc	1388
Leu Ser Ala Val Val Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala	
445	450 455
agt ggc ttc tgg agc agc ctg gtg aac cct gcc aca ggc ctg gct gag	1436
Ser Gly Phe Trp Ser Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu	
460	465 470 475
gtg gaa gga gaa aat gcc cag cgt tac ttc gat gcc ctg ctg aaa ttg	1484
Val Glu Gly Glu Asn Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu	
480	485 490
cga cag gag cgt ggg atg ggt gag gac ttc ctg agc tgg aat gac ctg	1532
Arg Gln Glu Arg Gly Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu	
495	500 505
cag gcc acc gtg agc cag gtc aat gca cag acc cag gaa gag act gac	1580
Gln Ala Thr Val Ser Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp	
510	515 520
cgg gtc ctt gca gtc agc ctc atc aat gag gct ctg gac aaa ggc agc	1628

Sequence Listing

Arg Val Leu Ala Val Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser	
525	530 535
cct gag aag act ctg tct gcc cta ctg ctt cct gca gct ggc cta gat	1676
Pro Glu Lys Thr Leu Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp	
540	545 550 555
gat gtc agc ctc cct gtc gcc cct cgg tac cat ctc ctc ctt gtg gca	1724
Asp Val Ser Leu Pro Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala	
560	565 570
gcc aaa agg cag aag gcc cag gtg aca ggg gat cct gga gct gtg ctg	1772
Ala Lys Arg Gln Lys Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu	
575	580 585
tgg ctt gag gag atc cgc cag gga gtg gtc aga gcc aac cag gac act	1820
Trp Leu Glu Glu Ile Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr	
590	595 600
aat aca gct cag aga atg gct ctt ggt gtg gct gcc atc aat caa gcc	1868
Asn Thr Ala Gln Arg Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala	
605	610 615
atc aag gag ggc aag gca gcc cag act gag cgg gtg ttg agg aac ccc	1916
Ile Lys Glu Gly Lys Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro	
620	625 630 635
gca gtg gcc ctt cga ggg gta gtt ccc gac tgt gcc aac ggc tac cag	1964
Ala Val Ala Leu Arg Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln	
640	645 650
cga gcc ctg gaa agt gcc atg gca aag aaa cag cgt cca gca gac aca	2012
Arg Ala Leu Glu Ser Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr	
655	660 665
gct ttc tgg gtt caa cat gac atg aag gat ggc act gcc tac tac ttc	2060
Ala Phe Trp Val Gln His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe	
670	675 680
cat ctg cag acc ttc cag ggg atc tgg gag caa cct cct ggc tgc ccc	2108

Sequence Listing

His Leu Gln Thr Phe Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro	
685	690 695
ctc aac acc tct cac ctg acc cgg gag gag atc cag tca gct gtc acc	2156
Leu Asn Thr Ser His Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr	
700	705 710 715
aag gtc act gct gcc tat gac cgc caa cag ctc tgg aaa gcc aac gtc	2204
Lys Val Thr Ala Ala Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val	
	720 725 730
ggc ttt gtt atc cag ctc cag gcc cgc ctc cgt ggc ttc cta gtt cgg	2252
Gly Phe Val Ile Gln Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg	
	735 740 745
cag aag ttt gct gag cat tcc cac ttt ctg agg acc tgg ctc cca gca	2300
Gln Lys Phe Ala Glu His Ser His Phe Leu Arg Thr Trp Leu Pro Ala	
	750 755 760
gtc atc aag atc cag gct cat tgg cgg ggt tat agg cag cgg aag att	2348
Val Ile Lys Ile Gln Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile	
	765 770 775
tac ctg gag tgg ttg cag tat ttt aaa gca aac ctg gat gcc ata atc	2396
Tyr Leu Glu Trp Leu Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile	
	780 785 790 795
aag atc cag gcc tgg gcc cgg atg tgg gca gct cgg agg caa tac ctg	2444
Lys Ile Gln Ala Trp Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu	
	800 805 810
agg cgt ctg cac tac ttc cag aag aat gtt aac tcc att gtg aag atc	2492
Arg Arg Leu His Tyr Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile	
	815 820 825
cag gca ttt ttc cga gcc agg aaa gcc caa gat gac tac agg ata tta	2540
Gln Ala Phe Phe Arg Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu	
	830 835 840
gtg cat gca ccc cac cct cct ctc agt gtg gta cgc aga ttt gcc cat	2588

Sequence Listing

Val His Ala Pro His Pro Pro Leu Ser Val Val Arg Arg Phe Ala His	
845	850 855
ctc ttg aat caa agc cag caa gac ttc ttg gct gag gca gag ctg ctg	2636
Leu Leu Asn Gln Ser Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu	
860	865 870 875
aag ctc cag gaa gag gta gtt agg aag atc cga tcc aat cag cag ctg	2684
Lys Leu Gln Glu Glu Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu	
	880 885 890
gag cag gac ctc aac atc atg gac atc aag att ggc ctg ctg gtg aag	2732
Glu Gln Asp Leu Asn Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys	
	895 900 905
aac cgg atc act ctg cag gaa gtg gtc tcc cac tgc aag aag ctg acc	2780
Asn Arg Ile Thr Leu Gln Glu Val Val Ser His Cys Lys Lys Leu Thr	
	910 915 920
aag agg aat aag gaa cag ctg tca gat atg atg gtt ctg gac aag cag	2828
Lys Arg Asn Lys Glu Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln	
	925 930 935
aag ggt tta aag tcg ctg agc aaa gag aaa cgg cag aaa cta gaa gca	2876
Lys Gly Leu Lys Ser Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala	
940	945 950 955
tac caa cac ctc ttc tac ctg ctc cag act cag ccc atc tac ctg gcc	2924
Tyr Gln His Leu Phe Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala	
	960 965 970
aag ctg atc ttt cag atg cca cag aac aaa acc acc aag ttc atg gag	2972
Lys Leu Ile Phe Gln Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu	
	975 980 985
gca gtg att ttc agc ctg tac aac tat gcc tcc agc cgc cga gag gcc	3020
Ala Val Ile Phe Ser Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala	
	990 995 1000
tat ctc ctg ctc cag ctg ttc aag aca gca ctc cag gag gaa atc aag	3068

Sequence Listing

Tyr Leu Leu Leu Gln Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys
 1005 1010 1015

tca aag gtg gag cag ccc cag gac gtg gtg aca ggc aac cca aca gtg 3116
 Ser Lys Val Glu Gln Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val
 1020 1025 1030 1035

gtg agg ctg gtg gtg aga ttc tac cgt aat ggg cgg gga cag agt gcc 3164
 Val Arg Leu Val Val Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala
 1040 1045 1050

ctg cag gag att ctg ggc aag gtt atc cag gat gtg cta gaa gac aaa 3212
 Leu Gln Glu Ile Leu Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys
 1055 1060 1065

gtg ctc agc gtc cac aca gac cct gtc cac ctc tat aag aac tgg atc 3260
 Val Leu Ser Val His Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile
 1070 1075 1080

aac cag act gag gcc cag aca ggg cag cgc agc cat ctc cca tat gat 3308
 Asn Gln Thr Glu Ala Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp
 1085 1090 1095

gtc acc ccg gag cag gcc ttg agc cac ccc gag gtc cag aga cga ctg 3356
 Val Thr Pro Glu Gln Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu
 1100 1105 1110 1115

gac atc gcc cta cgc aac ctc ctc gcc atg act gat aag ttc ctt tta 3404
 Asp Ile Ala Leu Arg Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu
 1120 1125 1130

gcc atc acc tca tct gtg gac caa att ccg tat ggg atg cga tat gtg 3452
 Ala Ile Thr Ser Ser Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val
 1135 1140 1145

gcc aaa gtc ctg aag gca act ctg gca gag aaa ttc cct gac gcc aca 3500
 Ala Lys Val Leu Lys Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr
 1150 1155 1160

gac agc gag gtc tat aag gtg gtc ggg aac ctc ctg tac tac cgc ttc 3548

Sequence Listing

Asp Ser Glu Val Tyr Lys Val Val Gly Asn Leu Leu Tyr Tyr Arg Phe	
1165	1170 1175
ctg aac cca gct gtg gtg gct cct gac gcc ttc gac att gtg gcc atg	3596
Leu Asn Pro Ala Val Val Ala Pro Asp Ala Phe Asp Ile Val Ala Met	
1180	1185 1190 1195
gca gct ggt gga gcc ctg gct gcc ccc cag cgc cat gcc ctg ggg gct	3644
Ala Ala Gly Gly Ala Leu Ala Ala Pro Gln Arg His Ala Leu Gly Ala	
1200	1205 1210
gtg gct cag ctc cta cag cac gct gcg gct ggc aag gcc ttc tct ggg	3692
Val Ala Gln Leu Leu Gln His Ala Ala Ala Gly Lys Ala Phe Ser Gly	
1215	1220 1225
cag agc cag cac cta cgg gtc ctg aat gac tat ctg gag gaa aca cac	3740
Gln Ser Gln His Leu Arg Val Leu Asn Asp Tyr Leu Glu Glu Thr His	
1230	1235 1240
ctc aag ttc agg aag ttc atc cat aga gcc tgc cag gtg cca gag cca	3788
Leu Lys Phe Arg Lys Phe Ile His Arg Ala Cys Gln Val Pro Glu Pro	
1245	1250 1255
gag gag cgt ttt gca gtg gac gag tac tca gac atg gtg gct gtg gcc	3836
Glu Glu Arg Phe Ala Val Asp Glu Tyr Ser Asp Met Val Ala Val Ala	
1260	1265 1270 1275
aaa ccc atg gtg tac atc acc gtg ggg gag ctg gtc aac acg cac agg	3884
Lys Pro Met Val Tyr Ile Thr Val Gly Glu Leu Val Asn Thr His Arg	
1280	1285 1290
ctg ttg ctg gag cac cag gac tgc att gcc cct gat cac caa gac ccc	3932
Leu Leu Leu Glu His Gln Asp Cys Ile Ala Pro Asp His Gln Asp Pro	
1295	1300 1305
ctg cat gag ctc ctg gag gat ctt ggg gag ctg ccc acc atc cct gac	3980
Leu His Glu Leu Leu Glu Asp Leu Gly Glu Leu Pro Thr Ile Pro Asp	
1310	1315 1320
ctt att ggt gag agc atc gct gca gat ggg cac aca gac ctg agc aag	4028

Sequence Listing

Leu Ile Gly Glu Ser Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys	
1325	1330 1335
cta gaa gtg tcc ctg acg ctg acc aac aag ttt gaa gga cta gag gca	4076
Leu Glu Val Ser Leu Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala	
1340	1345 1350 1355
gat gct gat gac tcc aac acc cgt agc ctg ctt ctg agc acc aag cag	4124
Asp Ala Asp Asp Ser Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln	
1360	1365 1370
ctg ttg gcc gat atc ata cag ttc cat cct ggg gac acc ctc aag gag	4172
Leu Leu Ala Asp Ile Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu	
1375	1380 1385
atc ctg tcc ctc tcg gct tcc aga gag caa gaa gca gcc cac aag cag	4220
Ile Leu Ser Leu Ser Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln	
1390	1395 1400
ctg atg agc cga cgc cag gcc tgt aca gcc cag aca ccg gag cca ctg	4268
Leu Met Ser Arg Arg Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu	
1405	1410 1415
cga cga cac cgc tca ctg aca gct cac tcc ctc ctg cca ctg gca gag	4316
Arg Arg His Arg Ser Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu	
1420	1425 1430 1435
aag cag cgg cgc gtc ctg cgg aac ctg cgc cga ctt gaa gcc ctg ggg	4364
Lys Gln Arg Arg Val Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly	
1440	1445 1450
ttg gtc agc gcc aga aat ggc tac cag ggg cta gtg gac gag ctg gcc	4412
Leu Val Ser Ala Arg Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala	
1455	1460 1465
aag gac atc cgc aac cag cac aga cac agg cac agg cgg aag gca gag	4460
Lys Asp Ile Arg Asn Gln His Arg His Arg His Arg Arg Lys Ala Glu	
1470	1475 1480
ctg gtg aag ctg cag gcc aca tta cag ggc ctg agc act aag acc acc	4508

Sequence Listing

Leu Val Lys Leu Gln Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr
 1485 1490 1495

ttc tat gag gag cag ggt gac tac tac agc cag tac atc cgg gcc tgc 4556
 Phe Tyr Glu Glu Gln Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys
 1500 1505 1510 1515

ctg gac cac ctg gcc ccc gac tcc aag agt tct ggg aag ggg aag aag 4604
 Leu Asp His Leu Ala Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys
 1520 1525 1530

cag cct tct ctt cat tac act gct gct cag ctc ctg gaa aag ggt gtc 4652
 Gln Pro Ser Leu His Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val
 1535 1540 1545

ttg gtg gaa att gaa gat ctt ccc gcc tct cac ttc aga aac gtc atc 4700
 Leu Val Glu Ile Glu Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile
 1550 1555 1560

ttt gac atc acg ccg gga gat gag gca gga aag ttt gaa gta aat gcc 4748
 Phe Asp Ile Thr Pro Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala
 1565 1570 1575

aag ttc ctg ggt gtg gac atg gag cga ttt cag ctt cac tat cag gat 4796
 Lys Phe Leu Gly Val Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp
 1580 1585 1590 1595

ctc ctg cag ctc cag tat gag ggt gtg gct gtc atg aaa ctc ttc aac 4844
 Leu Leu Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn
 1600 1605 1610

aag gcc aaa gtc aat gtc aac ctt ctc atc ttc ctc ctc aac aag aag 4892
 Lys Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys
 1615 1620 1625

ttt ttg cgg aag tgacag aggcaaaggg tgctacccaa gccctctta 4940
 Phe Leu Arg Lys
 1630

cctctctgga tgctttcttt aacactaact caccactgtg cttccctgca gacacccaga 5000

Sequence Listing

gctcaggact gggcaaggcc cagggattct cacccttcc ccagctggga ggagcttgcc 5060
 tgccctggcca cagacagtgt atcttctaata tggctaaagt gggccttgcc cagagtcag 5120
 ctgtgtggct tttatcatgc atgacaaacc cctggcttcc ctgccagatg gattctcatc 5180
 ccttacagct gactcttcca ggcaatttcc atagatctgc agtcctgcct ctgccacagt 5240
 ctctctgttg tccccacatc tacccaactt cctgtactgt tgcccttctg atgttaataa 5300
 aagcagctgt tactccc 5317

<210> 4
 <211> 1631
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Glu Arg Arg Ala Ala Gly Pro Gly Trp Ala Ala Tyr Glu Arg Leu
 1 5 10 15
 Thr Ala Glu Glu Met Asp Glu Gln Arg Arg Gln Asn Val Ala Tyr Gln
 20 25 30
 Tyr Leu Cys Arg Leu Glu Glu Ala Lys Arg Trp Met Glu Ala Cys Leu
 35 40 45
 Lys Glu Glu Leu Pro Ser Pro Val Glu Leu Glu Glu Ser Leu Arg Asn
 50 55 60
 Gly Val Leu Leu Ala Lys Leu Gly His Cys Phe Ala Pro Ser Val Val
 65 70 75 80
 Pro Leu Lys Lys Ile Tyr Asp Val Glu Gln Leu Arg Tyr Gln Ala Thr
 85 90 95
 Gly Leu His Phe Arg His Thr Asp Asn Ile Asn Phe Trp Leu Ser Ala
 100 105 110

Sequence Listing

Ile Ala His Ile Gly Leu Pro Ser Thr Phe Phe Pro Glu Thr Thr Asp
 115 120 125

Ile Tyr Asp Lys Lys Asn Met Pro Arg Val Val Tyr Cys Ile His Ala
 130 135 140

Leu Ser Leu Phe Leu Phe Arg Leu Gly Leu Ala Pro Gln Ile His Asp
 145 150 155 160

Leu Tyr Gly Lys Val Lys Phe Thr Ala Glu Glu Leu Ser Asn Met Ala
 165 170 175

Ser Glu Leu Ala Lys Tyr Gly Leu Gln Leu Pro Ala Phe Ser Lys Ile
 180 185 190

Gly Gly Ile Leu Ala Asn Glu Leu Ser Val Asp Glu Ala Ala Val His
 195 200 205

Ala Ala Val Leu Ala Ile Asn Glu Ala Val Glu Arg Gly Val Val Glu
 210 215 220

Asp Thr Leu Ala Ala Leu Gln Asn Pro Ser Ala Leu Leu Glu Asn Leu
 225 230 235 240

Arg Glu Pro Leu Ala Ala Val Tyr Gln Glu Met Leu Ala Gln Ala Lys
 245 250 255

Met Glu Lys Ala Ala Asn Ala Arg Asn His Asp Asp Arg Glu Ser Gln
 260 265 270

Asp Ile Tyr Asp His Tyr Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile
 275 280 285

Asn His Val Asn Val His Gly Ala Leu Glu Val Val Asp Asp Ala Leu
 290 295 300

Glu Arg Gln Ser Pro Glu Ala Leu Leu Lys Ala Leu Gln Asp Pro Ala
 305 310 315 320

Sequence Listing

Leu Ala Leu Arg Gly Val Arg Arg Asp Phe Ala Asp Trp Tyr Leu Glu
325 330 335

Gln Leu Asn Ser Asp Arg Glu Gln Lys Ala Gln Glu Leu Gly Leu Val
340 345 350

Glu Leu Leu Glu Lys Glu Glu Val Gln Ala Gly Val Ala Ala Ala Asn
355 360 365

Thr Lys Gly Asp Gln Glu Gln Ala Met Leu His Ala Val Gln Arg Ile
370 375 380

Asn Lys Ala Ile Arg Arg Gly Val Ala Ala Asp Thr Val Lys Glu Leu
385 390 395 400

Met Cys Pro Glu Ala Gln Leu Pro Pro Val Tyr Pro Val Ala Ser Ser
405 410 415

Met Tyr Gln Leu Glu Leu Ala Val Leu Gln Gln Gln Gln Gly Glu Leu
420 425 430

Gly Gln Glu Glu Leu Phe Val Ala Val Glu Met Leu Ser Ala Val Val
435 440 445

Leu Ile Asn Arg Ala Leu Glu Ala Arg Asp Ala Ser Gly Phe Trp Ser
450 455 460

Ser Leu Val Asn Pro Ala Thr Gly Leu Ala Glu Val Glu Gly Glu Asn
465 470 475 480

Ala Gln Arg Tyr Phe Asp Ala Leu Leu Lys Leu Arg Gln Glu Arg Gly
485 490 495

Met Gly Glu Asp Phe Leu Ser Trp Asn Asp Leu Gln Ala Thr Val Ser
500 505 510

Gln Val Asn Ala Gln Thr Gln Glu Glu Thr Asp Arg Val Leu Ala Val
515 520 525

Ser Leu Ile Asn Glu Ala Leu Asp Lys Gly Ser Pro Glu Lys Thr Leu

Sequence Listing

530	535	540	
Ser Ala Leu Leu Leu Pro Ala Ala Gly Leu Asp Asp Val Ser Leu Pro			
545	550	555	560
Val Ala Pro Arg Tyr His Leu Leu Leu Val Ala Ala Lys Arg Gln Lys			
565	570	575	
Ala Gln Val Thr Gly Asp Pro Gly Ala Val Leu Trp Leu Glu Glu Ile			
580	585	590	
Arg Gln Gly Val Val Arg Ala Asn Gln Asp Thr Asn Thr Ala Gln Arg			
595	600	605	
Met Ala Leu Gly Val Ala Ala Ile Asn Gln Ala Ile Lys Glu Gly Lys			
610	615	620	
Ala Ala Gln Thr Glu Arg Val Leu Arg Asn Pro Ala Val Ala Leu Arg			
625	630	635	640
Gly Val Val Pro Asp Cys Ala Asn Gly Tyr Gln Arg Ala Leu Glu Ser			
645	650	655	
Ala Met Ala Lys Lys Gln Arg Pro Ala Asp Thr Ala Phe Trp Val Gln			
660	665	670	
His Asp Met Lys Asp Gly Thr Ala Tyr Tyr Phe His Leu Gln Thr Phe			
675	680	685	
Gln Gly Ile Trp Glu Gln Pro Pro Gly Cys Pro Leu Asn Thr Ser His			
690	695	700	
Leu Thr Arg Glu Glu Ile Gln Ser Ala Val Thr Lys Val Thr Ala Ala			
705	710	715	720
Tyr Asp Arg Gln Gln Leu Trp Lys Ala Asn Val Gly Phe Val Ile Gln			
725	730	735	
Leu Gln Ala Arg Leu Arg Gly Phe Leu Val Arg Gln Lys Phe Ala Glu			
740	745	750	

Sequence Listing

His Ser His Phe Leu Arg Thr Trp Leu Pro Ala Val Ile Lys Ile Gln
755 760 765

Ala His Trp Arg Gly Tyr Arg Gln Arg Lys Ile Tyr Leu Glu Trp Leu
770 775 780

Gln Tyr Phe Lys Ala Asn Leu Asp Ala Ile Ile Lys Ile Gln Ala Trp
785 790 795 800

Ala Arg Met Trp Ala Ala Arg Arg Gln Tyr Leu Arg Arg Leu His Tyr
805 810 815

Phe Gln Lys Asn Val Asn Ser Ile Val Lys Ile Gln Ala Phe Phe Arg
820 825 830

Ala Arg Lys Ala Gln Asp Asp Tyr Arg Ile Leu Val His Ala Pro His
835 840 845

Pro Pro Leu Ser Val Val Arg Arg Phe Ala His Leu Leu Asn Gln Ser
850 855 860

Gln Gln Asp Phe Leu Ala Glu Ala Glu Leu Leu Lys Leu Gln Glu Glu
865 870 875 880

Val Val Arg Lys Ile Arg Ser Asn Gln Gln Leu Glu Gln Asp Leu Asn
885 890 895

Ile Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Arg Ile Thr Leu
900 905 910

Gln Glu Val Val Ser His Cys Lys Lys Leu Thr Lys Arg Asn Lys Glu
915 920 925

Gln Leu Ser Asp Met Met Val Leu Asp Lys Gln Lys Gly Leu Lys Ser
930 935 940

Leu Ser Lys Glu Lys Arg Gln Lys Leu Glu Ala Tyr Gln His Leu Phe
945 950 955 960

Sequence Listing

Tyr Leu Leu Gln Thr Gln Pro Ile Tyr Leu Ala Lys Leu Ile Phe Gln
 965 970 975

Met Pro Gln Asn Lys Thr Thr Lys Phe Met Glu Ala Val Ile Phe Ser
 980 985 990

Leu Tyr Asn Tyr Ala Ser Ser Arg Arg Glu Ala Tyr Leu Leu Gln
 995 1000 1005

Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val Glu Gln
 1010 1015 1020

Pro Gln Asp Val Val Thr Gly Asn Pro Thr Val Val Arg Leu Val Val
 1025 1030 1035 1040

Arg Phe Tyr Arg Asn Gly Arg Gly Gln Ser Ala Leu Gln Glu Ile Leu
 1045 1050 1055

Gly Lys Val Ile Gln Asp Val Leu Glu Asp Lys Val Leu Ser Val His
 1060 1065 1070

Thr Asp Pro Val His Leu Tyr Lys Asn Trp Ile Asn Gln Thr Glu Ala
 1075 1080 1085

Gln Thr Gly Gln Arg Ser His Leu Pro Tyr Asp Val Thr Pro Glu Gln
 1090 1095 1100

Ala Leu Ser His Pro Glu Val Gln Arg Arg Leu Asp Ile Ala Leu Arg
 1105 1110 1115 1120

Asn Leu Leu Ala Met Thr Asp Lys Phe Leu Leu Ala Ile Thr Ser Ser
 1125 1130 1135

Val Asp Gln Ile Pro Tyr Gly Met Arg Tyr Val Ala Lys Val Leu Lys
 1140 1145 1150

Ala Thr Leu Ala Glu Lys Phe Pro Asp Ala Thr Asp Ser Glu Val Tyr
 1155 1160 1165

Lys Val Val Gly Asn Leu Leu Tyr Tyr Arg Phe Leu Asn Pro Ala Val

Sequence Listing

1170	1175	1180	
Val Ala Pro Asp Ala Phe Asp Ile Val Ala Met Ala Ala Gly Gly Ala			
1185	1190	1195	1200
Leu Ala Ala Pro Gln Arg His Ala Leu Gly Ala Val Ala Gln Leu Leu			
1205	1210	1215	
Gln His Ala Ala Ala Gly Lys Ala Phe Ser Gly Gln Ser Gln His Leu			
1220	1225	1230	
Arg Val Leu Asn Asp Tyr Leu Glu Glu Thr His Leu Lys Phe Arg Lys			
1235	1240	1245	
Phe Ile His Arg Ala Cys Gln Val Pro Glu Pro Glu Glu Arg Phe Ala			
1250	1255	1260	
Val Asp Glu Tyr Ser Asp Met Val Ala Val Ala Lys Pro Met Val Tyr			
1265	1270	1275	1280
Ile Thr Val Gly Glu Leu Val Asn Thr His Arg Leu Leu Leu Glu His			
1285	1290	1295	
Gln Asp Cys Ile Ala Pro Asp His Gln Asp Pro Leu His Glu Leu Leu			
1300	1305	1310	
Glu Asp Leu Gly Glu Leu Pro Thr Ile Pro Asp Leu Ile Gly Glu Ser			
1315	1320	1325	
Ile Ala Ala Asp Gly His Thr Asp Leu Ser Lys Leu Glu Val Ser Leu			
1330	1335	1340	
Thr Leu Thr Asn Lys Phe Glu Gly Leu Glu Ala Asp Ala Asp Asp Ser			
1345	1350	1355	1360
Asn Thr Arg Ser Leu Leu Leu Ser Thr Lys Gln Leu Leu Ala Asp Ile			
1365	1370	1375	
Ile Gln Phe His Pro Gly Asp Thr Leu Lys Glu Ile Leu Ser Leu Ser			
1380	1385	1390	

Sequence Listing

Ala Ser Arg Glu Gln Glu Ala Ala His Lys Gln Leu Met Ser Arg Arg
 1395 1400 1405

Gln Ala Cys Thr Ala Gln Thr Pro Glu Pro Leu Arg Arg His Arg Ser
 1410 1415 1420

Leu Thr Ala His Ser Leu Leu Pro Leu Ala Glu Lys Gln Arg Arg Val
 1425 1430 1435 1440

Leu Arg Asn Leu Arg Arg Leu Glu Ala Leu Gly Leu Val Ser Ala Arg
 1445 1450 1455

Asn Gly Tyr Gln Gly Leu Val Asp Glu Leu Ala Lys Asp Ile Arg Asn
 1460 1465 1470

Gln His Arg His Arg His Arg Arg Lys Ala Glu Leu Val Lys Leu Gln
 1475 1480 1485

Ala Thr Leu Gln Gly Leu Ser Thr Lys Thr Thr Phe Tyr Glu Glu Gln
 1490 1495 1500

Gly Asp Tyr Tyr Ser Gln Tyr Ile Arg Ala Cys Leu Asp His Leu Ala
 1505 1510 1515 1520

Pro Asp Ser Lys Ser Ser Gly Lys Gly Lys Lys Gln Pro Ser Leu His
 1525 1530 1535

Tyr Thr Ala Ala Gln Leu Leu Glu Lys Gly Val Leu Val Glu Ile Glu
 1540 1545 1550

Asp Leu Pro Ala Ser His Phe Arg Asn Val Ile Phe Asp Ile Thr Pro
 1555 1560 1565

Gly Asp Glu Ala Gly Lys Phe Glu Val Asn Ala Lys Phe Leu Gly Val
 1570 1575 1580

Asp Met Glu Arg Phe Gln Leu His Tyr Gln Asp Leu Leu Gln Leu Gln
 1585 1590 1595 1600

Sequence Listing

Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asn Lys Ala Lys Val Asn
 1605 1610 1615

Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys Phe Leu Arg Lys
 1620 1625 1630

<210> 5
 <211> 3608
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (424) .. (1908)
 <223> Clone LBF1110

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 cctcagaaca tctcctgata gctacccagg accaggcacc aaggacaggg agtcccaggc 120
 gcacaccccc cattctgggt cccccaggcc cagacccccca ctctgccaca ggttgcatct 180
 tgacctggtc ctctgcaga agtggcccct gtggctcctgc tctgagactc gtccttgggc 240
 gccctgcag cccctttcta tgactccatc tggatttggc tggctgtggg gacgcggtcc 300
 gaggggaggg ctggctctca gcgtgggtggc agccagctct ctggccacca tggcaaatgc 360
 tgagatctga ggggacaagg ctctacagcc tcagccaggg gcactcagct gttgcagggt 420
 gtg atg gag aac aaa gct atg tac cta cac acc gtc agc gac tgt 465
 Met Glu Asn Lys Ala Met Tyr Leu His Thr Val Ser Asp Cys
 1 5 10
 gac acc agc tcc atc tgt gag gat tcc ttt gat ggc agg agc ctg tcc 513

Sequence Listing

Asp Thr Ser Ser Ile Cys Glu Asp Ser Phe Asp Gly Arg Ser Leu Ser	
15 20 25 30	
aag ctg aac ctg tgt gag gat ggt cca tgt cac aaa cgg cgg gca agc	561
Lys Leu Asn Leu Cys Glu Asp Gly Pro Cys His Lys Arg Arg Ala Ser	
35 40 45	
atc tgc tgt acc cag ctg ggg tcc ctg tcg gcc ctg aag cat gct gtc	609
Ile Cys Cys Thr Gln Leu Gly Ser Leu Ser Ala Leu Lys His Ala Val	
50 55 60	
ctg ggg ctc tac ctg ctg gtc ttc ctg att ctt gtg ggc atc ttc atc	657
Leu Gly Leu Tyr Leu Leu Val Phe Leu Ile Leu Val Gly Ile Phe Ile	
65 70 75	
tta gca gtg tcc agg ccg cgc agc tcc cct gac gac ctg aag gcc ctg	705
Leu Ala Val Ser Arg Pro Arg Ser Ser Pro Asp Asp Leu Lys Ala Leu	
80 85 90	
act cgc aat gtg aac cgg ctg aat gag agc ttc cgg gac ttg cag ctg	753
Thr Arg Asn Val Asn Arg Leu Asn Glu Ser Phe Arg Asp Leu Gln Leu	
95 100 105 110	
cgg ctg ctg cag gct ccg ctg caa gcg gac ctg acg gag cag gtg tgg	801
Arg Leu Leu Gln Ala Pro Leu Gln Ala Asp Leu Thr Glu Gln Val Trp	
115 120 125	
aag gtg cag gac gcg ctg cag aac cag tca gac tcg ttg ctg gcg ctg	849
Lys Val Gln Asp Ala Leu Gln Asn Gln Ser Asp Ser Leu Leu Ala Leu	
130 135 140	
gcg ggc gca gtg cag cgg ctg gag ggc gcg ctg tgg ggg ctg cag gcg	897
Ala Gly Ala Val Gln Arg Leu Glu Gly Ala Leu Trp Gly Leu Gln Ala	
145 150 155	
cag gcg gtg cag acc gag cag gcg gtg gcc ctg ctg cgg gac cgc acg	945
Gln Ala Val Gln Thr Glu Gln Ala Val Ala Leu Leu Arg Asp Arg Thr	
160 165 170	
qqc caq caq agc gac acg gcg cag ctg gag ctc tac cag ctg cag gtg	993

Sequence Listing

Gly	Gln	Gln	Ser	Asp	Thr	Ala	Gln	Leu	Glu	Leu	Tyr	Gln	Leu	Gln	Val		
175						180				185					190		
gag	agc	aac	agt	agc	cag	ctg	ctg	ctg	agg	cgc	cac	gcg	ggc	ctg	ctg		1041
Glu	Ser	Asn	Ser	Ser	Gln	Leu	Leu	Leu	Arg	Arg	His	Ala	Gly	Leu	Leu		
				195					200					205			
gac	ggg	ctg	gcg	cgc	agg	gtg	ggc	atc	ctg	ggc	gag	gag	ctg	gcc	gac		1089
Asp	Gly	Leu	Ala	Arg	Arg	Val	Gly	Ile	Leu	Gly	Glu	Glu	Leu	Ala	Asp		
			210					215					220				
gtg	ggc	ggc	gtg	ctg	cgc	ggc	ctc	aac	cac	agc	ctg	tcc	tac	gac	gtg		1137
Val	Gly	Gly	Val	Leu	Arg	Gly	Leu	Asn	His	Ser	Leu	Ser	Tyr	Asp	Val		
			225				230						235				
gcc	ctc	cac	cgc	acg	cgg	ctg	cag	gac	ctg	cgg	gtg	ctg	gtg	agc	aac		1185
Ala	Leu	His	Arg	Thr	Arg	Leu	Gln	Asp	Leu	Arg	Val	Leu	Val	Ser	Asn		
			240				245				250						
gcc	agc	gag	gac	acg	cgc	cgc	ctg	cgc	ctg	gcg	cac	gta	ggc	atg	gag		1233
Ala	Ser	Glu	Asp	Thr	Arg	Arg	Leu	Arg	Leu	Ala	His	Val	Gly	Met	Glu		
255						260				265					270		
ctg	cag	ctg	aag	cag	gag	ctg	gcc	atg	ctc	aac	gcg	gtc	acc	gag	gac		1281
Leu	Gln	Leu	Lys	Gln	Glu	Leu	Ala	Met	Leu	Asn	Ala	Val	Thr	Glu	Asp		
				275					280					285			
ctg	cgc	ctc	aag	gac	tgg	gag	cac	tcc	atc	gca	ctg	cgg	aac	atc	tcc		1329
Leu	Arg	Leu	Lys	Asp	Trp	Glu	His	Ser	Ile	Ala	Leu	Arg	Asn	Ile	Ser		
			290					295					300				
ctc	gcg	aaa	ggg	cca	ccg	gga	ccc	aaa	ggg	gat	cag	ggg	cat	gaa	gga		1377
Leu	Ala	Lys	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Asp	Gln	Gly	His	Glu	Gly		
			305				310					315					
aag	gaa	ggc	agg	cct	ggc	atc	cct	gga	ttg	cct	gga	ctt	cga	ggg	ctg		1425
Lys	Glu	Gly	Arg	Pro	Gly	Ile	Pro	Gly	Leu	Pro	Gly	Leu	Arg	Gly	Leu		
			320				325				330						
ccc	ggg	gag	aga	ggg	acc	cca	gga	ttg	ccc	ggg	ccc	aag	ggc	gat	gat		1473

Sequence Listing

Pro Gly Glu Arg Gly Thr	Pro Gly Leu	Pro Gly Pro Lys Gly Asp Asp	
335	340	345	350
ggg aag ctg ggg gcc aca gga cca atg ggc atg cgt ggg ttc aaa ggt			1521
Gly Lys Leu Gly Ala Thr Gly Pro Met Gly Met Arg Gly Phe Lys Gly			
355	360	365	
gac cga ggc cca aaa gga gag aaa gga gag aaa gga gac aga gct ggg			1569
Asp Arg Gly Pro Lys Gly Glu Lys Gly Glu Lys Gly Asp Arg Ala Gly			
370	375	380	
gat gcc agt ggc gtg gag gcc ccg atg atg atc cgc ctg gtg aat ggc			1617
Asp Ala Ser Gly Val Glu Ala Pro Met Met Ile Arg Leu Val Asn Gly			
385	390	395	
tca ggt ccg cac gag ggc cgc gtg gaa gtg tac cac gac cgg cgt tgg			1665
Ser Gly Pro His Glu Gly Arg Val Glu Val Tyr His Asp Arg Arg Trp			
400	405	410	
ggc acc gtg tgt gac gac ggc tgg gac aag aag gac gga gac gtg gtg			1713
Gly Thr Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val			
415	420	425	430
tgc cgc atg ctc ggc ttc cgc ggt gtg gag gag gtg tac cgc aca gct			1761
Cys Arg Met Leu Gly Phe Arg Gly Val Glu Glu Val Tyr Arg Thr Ala			
435	440	445	
cga ttc ggg caa ggc act ggg agg atc tgg atg gat gac gtt gcc tgc			1809
Arg Phe Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Ala Cys			
450	455	460	
aag ggc aca gag gaa acc atc ttc cgc tgc agc ttc tcc aaa tgg ggg			1857
Lys Gly Thr Glu Glu Thr Ile Phe Arg Cys Ser Phe Ser Lys Trp Gly			
465	470	475	
gtg aca aac tgt gga cat gcc gaa gat gcc agc gtg aca tgc aac aga			1905
Val Thr Asn Cys Gly His Ala Glu Asp Ala Ser Val Thr Cys Asn Arg			
480	485	490	
cac	tg aaagtgggca gagcccaagt tcggggctcct qcacagaqca cccttcctgc		1960

Sequence Listing

His

495

atccctgggg tggggcacag ctcggggcca ccctgaccat gcctcgacca caccctgtcc	2020
agcattctca gtcttcacac ctgcatccca ggaccgtggg ggccggtcgt catttccctc	2080
ttgaacatgt gctccgaagt ataactctgg gacctactgc ccgtctctct cttccaccag	2140
gttcctgcat gaggagccct gatcaactgg atcaccactt tgcccagcct ctgaacacca	2200
tgcaccaggc ctcaatatcc cagttccctt tggcctttta gttacagggt aatgctgaga	2260
atgtgtcaga gacaagtgca gcagcagcga tggttggtag tatagatcat ttactcttca	2320
gacaattccc aaacctccat tagtccaaga gtttctacat ctctctcccc agcaagaggc	2380
aacgtcaagt gatgaatttc ccccttttac tctgcctctg ctccccattt gctagtttga	2440
ggaagtgaca tagaggagaa gccagctgta ggggcaagag ggaaatgcaa gtcacctgca	2500
ggaatccagc tagatttgga gaagggaatg aaactaacat tgaatgacta ccatggcacg	2560
ctaaatagta tcttggtgtc caaattcatg tatccactta gctgcattgg tccagggcct	2620
gtcagtctgg atacagcctt acctccagggt agcacttaac tggtcattc acctagactg	2680
caagtaagaa gacaaaatga ctgagaccgt gtgcccacct gaacttattg tctttacttg	2740
gcctgagcta aaagcttggg tgcaggacct gtgtaactag aaagttgcct acttcagaac	2800
ctccagggcg tgagtgaag gtcaaacatg actggcttcc aggccgacca tcaatgtagg	2860
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ctggcattgg gcagtcacgg ttaaagccaa gtcattgtgt tctcagctgt ttggagggtga	2980
tgattttgca tcttccaagc ctcttcagggt gtgaatctgt ggtcaggaaa acacaagtcc	3040
taatggaacc cttagggggg aaggaaatga agattcccta taacctctgg ggggtggggag	3100

Sequence Listing

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taggaataag gggcttgggc ctccataaat ctgcaatctg caccctcctc ctagagacag      3160
ggagatcgtg ttctgctttt tacatgagga gcagaactgg gccatacaca tgttcaagaa      3220
ctagggggagc tacctggtag caagtgagtg cagacccacc tcaccttggg ggaatctcaa      3280
actcataggc ctcagataca cgatcacctg tcatatcagg tgagcactgg cctgcttggg      3340
gagagacctg ggcccctcca ggtgtaggaa cagcaacact cctggctgac aactaagcca      3400
atatggccct aggtcattct tgcttccaat atgcttgcca ctcccttaa gtcctaata      3460
tgagaaactc tctttctgac caattgctat gtttacataa cacgcatgta ctcatgcatc      3520
ccttgccaga gccatatat gtatgcatat ataaacatag cactttttac tacatagctc      3580
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<210> 6

<211> 495

<212> PRT

<213> Homo sapiens

<400> 6

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Met Glu Asn Lys Ala Met Tyr Leu His Thr Val Ser Asp Cys Asp Thr
  1             5             10             15

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Ser Ser Ile Cys Glu Asp Ser Phe Asp Gly Arg Ser Leu Ser Lys Leu
      20             25             30

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Asn Leu Cys Glu Asp Gly Pro Cys His Lys Arg Arg Ala Ser Ile Cys
      35             40             45

```

```

Cys Thr Gln Leu Gly Ser Leu Ser Ala Leu Lys His Ala Val Leu Gly
      50             55             60

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Leu Tyr Leu Leu Val Phe Leu Ile Leu Val Gly Ile Phe Ile Leu Ala
      65             70             75             80

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Sequence Listing

Val Ser Arg Pro Arg Ser Ser Pro Asp Asp Leu Lys Ala Leu Thr Arg
85 90 95

Asn Val Asn Arg Leu Asn Glu Ser Phe Arg Asp Leu Gln Leu Arg Leu
100 105 110

Leu Gln Ala Pro Leu Gln Ala Asp Leu Thr Glu Gln Val Trp Lys Val
115 120 125

Gln Asp Ala Leu Gln Asn Gln Ser Asp Ser Leu Leu Ala Leu Ala Gly
130 135 140

Ala Val Gln Arg Leu Glu Gly Ala Leu Trp Gly Leu Gln Ala Gln Ala
145 150 155 160

Val Gln Thr Glu Gln Ala Val Ala Leu Leu Arg Asp Arg Thr Gly Gln
165 170 175

Gln Ser Asp Thr Ala Gln Leu Glu Leu Tyr Gln Leu Gln Val Glu Ser
180 185 190

Asn Ser Ser Gln Leu Leu Leu Arg Arg His Ala Gly Leu Leu Asp Gly
195 200 205

Leu Ala Arg Arg Val Gly Ile Leu Gly Glu Glu Leu Ala Asp Val Gly
210 215 220

Gly Val Leu Arg Gly Leu Asn His Ser Leu Ser Tyr Asp Val Ala Leu
225 230 235 240

His Arg Thr Arg Leu Gln Asp Leu Arg Val Leu Val Ser Asn Ala Ser
245 250 255

Glu Asp Thr Arg Arg Leu Arg Leu Ala His Val Gly Met Glu Leu Gln
260 265 270

Leu Lys Gln Glu Leu Ala Met Leu Asn Ala Val Thr Glu Asp Leu Arg
275 280 285

Sequence Listing

Leu Lys Asp Trp Glu His Ser Ile Ala Leu Arg Asn Ile Ser Leu Ala
290 295 300

Lys Gly Pro Pro Gly Pro Lys Gly Asp Gln Gly His Glu Gly Lys Glu
305 310 315 320

Gly Arg Pro Gly Ile Pro Gly Leu Pro Gly Leu Arg Gly Leu Pro Gly
325 330 335

Glu Arg Gly Thr Pro Gly Leu Pro Gly Pro Lys Gly Asp Asp Gly Lys
340 345 350

Leu Gly Ala Thr Gly Pro Met Gly Met Arg Gly Phe Lys Gly Asp Arg
355 360 365

Gly Pro Lys Gly Glu Lys Gly Glu Lys Gly Asp Arg Ala Gly Asp Ala
370 375 380

Ser Gly Val Glu Ala Pro Met Met Ile Arg Leu Val Asn Gly Ser Gly
385 390 395 400

Pro His Glu Gly Arg Val Glu Val Tyr His Asp Arg Arg Trp Gly Thr
405 410 415

Val Cys Asp Asp Gly Trp Asp Lys Lys Asp Gly Asp Val Val Cys Arg
420 425 430

Met Leu Gly Phe Arg Gly Val Glu Glu Val Tyr Arg Thr Ala Arg Phe
435 440 445

Gly Gln Gly Thr Gly Arg Ile Trp Met Asp Asp Val Ala Cys Lys Gly
450 455 460

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465 470 475 480

Asn Cys Gly His Ala Glu Asp Ala Ser Val Thr Cys Asn Arg His
485 490 495

Sequence Listing

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 <213> Homo sapiens

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 <222> (405) .. (1835)
 <223> Clone LBFL123

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tgcccgccgc cgctgcgggt ctgtgggggc agagggcggc ggctcccagg gcagcgcgta	180
gcgggaccga ttgcctaata ctccggcagg ggccggggcc gcagctggct cggataaata	240
gccgcccggc tggcccgag ctgcagggga gagcggcggc cgcgatcccc accacaccac	300
cagcccggcc gcacggggca ctgagccggg tgctgagcac cggaggcccc gccgaggccg	360
ggactcagga cctgcagaga aacgcctcct gattttgtct taca atg gaa ctt	413
	Met Glu Leu
	1
aaa aag tcg cct gac ggt gga tgg ggc tgg gtg att gtg ttt gtc tcc	461
Lys Lys Ser Pro Asp Gly Gly Trp Gly Trp Val Ile Val Phe Val Ser	
5 10 15	
ttc ctt act cag ttt ttg tgt tac gga tcc cca cta gct gtt gga gtc	509
Phe Leu Thr Gln Phe Leu Cys Tyr Gly Ser Pro Leu Ala Val Gly Val	
20 25 30 35	
ctg tac ata gaa tgg ctg gat gcc ttt ggt gaa gga aaa gga aaa aca	557
Leu Tyr Ile Glu Trp Leu Asp Ala Phe Gly Glu Gly Lys Gly Lys Thr	
40 45 50	

Sequence Listing

gcc tgg gtt gga tcc ctg gca agt gga gtt ggc ttg ctt gca agt cct Ala Trp Val Gly Ser Leu Ala Ser Gly Val Gly Leu Leu Ala Ser Pro	605
55 60 65	
gtc tgc agt ctc tgt gtc tca tct ttt gga gca aga cct gtc aca atc Val Cys Ser Leu Cys Val Ser Ser Phe Gly Ala Arg Pro Val Thr Ile	653
70 75 80	
ttc agt ggc ttc atg gtg gct gga ggc ctg atg ttg agc agt ttt gct Phe Ser Gly Phe Met Val Ala Gly Gly Leu Met Leu Ser Ser Phe Ala	701
85 90 95	
ccc aat atc tac ttt ctg ttt ttt tcc tat ggc att gtt gta ggt tca Pro Asn Ile Tyr Phe Leu Phe Phe Ser Tyr Gly Ile Val Val Gly Ser	749
100 105 110 115	
agc gtt ggc ctt ttc ata tat gct gct ctg cag agg atg ctg gtt gag Ser Val Gly Leu Phe Ile Tyr Ala Ala Leu Gln Arg Met Leu Val Glu	797
120 125 130	
ttc tat gga ctg gat gga tgc ttg ctg att gtg ggt gct tta gct tta Phe Tyr Gly Leu Asp Gly Cys Leu Leu Ile Val Gly Ala Leu Ala Leu	845
135 140 145	
aat ata tta gcc tgt ggc agt ctg atg aga ccc ctc caa tct tct gat Asn Ile Leu Ala Cys Gly Ser Leu Met Arg Pro Leu Gln Ser Ser Asp	893
150 155 160	
tgt cct ttg cct aaa aaa ata gct cca gaa gat cta cca gat aaa tac Cys Pro Leu Pro Lys Lys Ile Ala Pro Glu Asp Leu Pro Asp Lys Tyr	941
165 170 175	
tcc att tac aat gaa aaa gga aag aat ctg gaa gaa aac ata aac att Ser Ile Tyr Asn Glu Lys Gly Lys Asn Leu Glu Glu Asn Ile Asn Ile	989
180 185 190 195	
ctt gac aag agc tac agt agt gag gaa aaa tgc agg atc acg tta gcc Leu Asp Lys Ser Tyr Ser Ser Glu Glu Lys Cys Arg Ile Thr Leu Ala	1037
200 205 210	

Sequence Listing

aat ggt gac tgg aaa caa gac agc cta ctt cat aaa aac ccc aca gtg	1085
Asn Gly Asp Trp Lys Gln Asp Ser Leu Leu His Lys Asn Pro Thr Val	
215 220 225	
aca cac aca aaa gag cct gaa acg tac aaa aag aaa gtt gca gaa cag	1133
Thr His Thr Lys Glu Pro Glu Thr Tyr Lys Lys Lys Val Ala Glu Gln	
230 235 240	
aca tat ttt tgc aaa cag ctt gcc aag agg aag tgg cag tta tat aaa	1181
Thr Tyr Phe Cys Lys Gln Leu Ala Lys Arg Lys Trp Gln Leu Tyr Lys	
245 250 255	
aac tac tgt ggt gaa act gtg gct ctt ttt aaa aac aaa gta ttt tca	1229
Asn Tyr Cys Gly Glu Thr Val Ala Leu Phe Lys Asn Lys Val Phe Ser	
260 265 270 275	
gcc ctt ttc att gct atc tta ctc ttt gac atc gga ggg ttt cca cct	1277
Ala Leu Phe Ile Ala Ile Leu Leu Phe Asp Ile Gly Gly Phe Pro Pro	
280 285 290	
tca tta ctt atg gaa gat gta gca aga agt tca aac gtg aaa gaa gaa	1325
Ser Leu Leu Met Glu Asp Val Ala Arg Ser Ser Asn Val Lys Glu Glu	
295 300 305	
gag ttt att atg cca ctt att tcc att ata ggc att atg aca gca gtt	1373
Glu Phe Ile Met Pro Leu Ile Ser Ile Ile Gly Ile Met Thr Ala Val	
310 315 320	
ggt aaa ctg ctt tta ggg ata ctg gct gac ttc aag tgg att aat acc	1421
Gly Lys Leu Leu Leu Gly Ile Leu Ala Asp Phe Lys Trp Ile Asn Thr	
325 330 335	
ttg tat ctt tat gtt gct acc tta atc atc atg ggc cta gcc ttg tgt	1469
Leu Tyr Leu Tyr Val Ala Thr Leu Ile Ile Met Gly Leu Ala Leu Cys	
340 345 350 355	
gca att cca ttt gcc aaa agc tat gtc aca ttg gcg ttg ctt tct ggg	1517
Ala Ile Pro Phe Ala Lys Ser Tyr Val Thr Leu Ala Leu Leu Ser Gly	
360 365 370	

Sequence Listing

atc cta ggg ttt ctt act ggt aat tgg tcc atc ttt cca tat gtg acc Ile Leu Gly Phe Leu Thr Gly Asn Trp Ser Ile Phe Pro Tyr Val Thr 375 380 385	1565
acg aag act gtg gga att gaa aaa tta gcc cat gcc tat ggg ata tta Thr Lys Thr Val Gly Ile Glu Lys Leu Ala His Ala Tyr Gly Ile Leu 390 395 400	1613
atg ttc ttt gct gga ctt gga aat agc cta gga cca ccc atc gtt ggt Met Phe Phe Ala Gly Leu Gly Asn Ser Leu Gly Pro Pro Ile Val Gly 405 410 415	1661
tgg ttt tat gac tgg acc cag acc tat gat att gca ttt tat ttt agt Trp Phe Tyr Asp Trp Thr Gln Thr Tyr Asp Ile Ala Phe Tyr Phe Ser 420 425 430 435	1709
ggc ttc tgc gtc ctg ctg gga ggt ttt att ctg ctg ctg gca gcc ttg Gly Phe Cys Val Leu Leu Gly Gly Phe Ile Leu Leu Leu Ala Ala Leu 440 445 450	1757
ccc tct tgg gat aca tgc aac aag caa ctc ccc aag cca gct cca aca Pro Ser Trp Asp Thr Cys Asn Lys Gln Leu Pro Lys Pro Ala Pro Thr 455 460 465	1805
act ttc ttg tac aaa gtt gcc tct aat gtt tagaa gaatattgga Thr Phe Leu Tyr Lys Val Ala Ser Asn Val 470 475	1850
agacactatt ttgctatatt tataccatat agcaacgata tttaacaga tctcaagcaa	1910
atcttctaga gtcaagacta ttttctcata gcaaaatttc acaatgactg actctgaatg	1970
aattattttt ttttttttat atatcctatt ttttatgtag tgtatgcgta gcctctatct	2030
cgtatttttt tctattttct ctccccacac catcaatggg actattctgt tttgctgtta	2090
ttcactagtt cttaacattg taataaagttt gaccagcctc agaaggcttt ctctgtgtaa	2150
agaagtataa tttctctgct gactccattt aatccactgc aaggcaccta gagagactgc	2210

Sequence Listing

tcctatttta aaagtgatgc aagcatcatg ataagatatg tgtgaagccc actaggaaat 2270
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taaaaaata tattttaacc tacagtcacc agttttcatt attctattta cctcactgaa 2450
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gcatgggata tgggaatgga aaagggcaat aagaaattaa taccottatg cagttgcatt 2930
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taaagaaatg ggttttaaac ttgggtatgc atcagaattc cctatagatc tttttgaaaa 3050
tataggtacc tgggtatcac acatagaact ttaattctg ctggtgtagg ctgttgccca 3110
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<211> 477

<212> PRT

<213> Homo sapiens

<400> 8

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Sequence Listing

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35	40	45	
Gly Lys Thr Ala Trp Val Gly Ser Leu Ala Ser Gly Val Gly Leu Leu			
50	55	60	
Ala Ser Pro Val Cys Ser Leu Cys Val Ser Ser Phe Gly Ala Arg Pro			
65	70	75	80
Val Thr Ile Phe Ser Gly Phe Met Val Ala Gly Gly Leu Met Leu Ser			
85	90	95	
Ser Phe Ala Pro Asn Ile Tyr Phe Leu Phe Phe Ser Tyr Gly Ile Val			
100	105	110	
Val Gly Ser Ser Val Gly Leu Phe Ile Tyr Ala Ala Leu Gln Arg Met			
115	120	125	
Leu Val Glu Phe Tyr Gly Leu Asp Gly Cys Leu Leu Ile Val Gly Ala			
130	135	140	
Leu Ala Leu Asn Ile Leu Ala Cys Gly Ser Leu Met Arg Pro Leu Gln			
145	150	155	160
Ser Ser Asp Cys Pro Leu Pro Lys Lys Ile Ala Pro Glu Asp Leu Pro			
165	170	175	
Asp Lys Tyr Ser Ile Tyr Asn Glu Lys Gly Lys Asn Leu Glu Glu Asn			
180	185	190	
Ile Asn Ile Leu Asp Lys Ser Tyr Ser Ser Glu Glu Lys Cys Arg Ile			
195	200	205	
Thr Leu Ala Asn Gly Asp Trp Lys Gln Asp Ser Leu Leu His Lys Asn			
210	215	220	

Sequence Listing

Pro Thr Val Thr His Thr Lys Glu Pro Glu Thr Tyr Lys Lys Lys Val
225 230 235 240

Ala Glu Gln Thr Tyr Phe Cys Lys Gln Leu Ala Lys Arg Lys Trp Gln
245 250 255

Leu Tyr Lys Asn Tyr Cys Gly Glu Thr Val Ala Leu Phe Lys Asn Lys
260 265 270

Val Phe Ser Ala Leu Phe Ile Ala Ile Leu Leu Phe Asp Ile Gly Gly
275 280 285

Phe Pro Pro Ser Leu Leu Met Glu Asp Val Ala Arg Ser Ser Asn Val
290 295 300

Lys Glu Glu Glu Phe Ile Met Pro Leu Ile Ser Ile Ile Gly Ile Met
305 310 315 320

Thr Ala Val Gly Lys Leu Leu Leu Gly Ile Leu Ala Asp Phe Lys Trp
325 330 335

Ile Asn Thr Leu Tyr Leu Tyr Val Ala Thr Leu Ile Ile Met Gly Leu
340 345 350

Ala Leu Cys Ala Ile Pro Phe Ala Lys Ser Tyr Val Thr Leu Ala Leu
355 360 365

Leu Ser Gly Ile Leu Gly Phe Leu Thr Gly Asn Trp Ser Ile Phe Pro
370 375 380

Tyr Val Thr Thr Lys Thr Val Gly Ile Glu Lys Leu Ala His Ala Tyr
385 390 395 400

Gly Ile Leu Met Phe Phe Ala Gly Leu Gly Asn Ser Leu Gly Pro Pro
405 410 415

Ile Val Gly Trp Phe Tyr Asp Trp Thr Gln Thr Tyr Asp Ile Ala Phe
420 425 430

Sequence Listing

Tyr Phe Ser Gly Phe Cys Val Leu Leu Gly Gly Phe Ile Leu Leu Leu
 435 440 445

Ala Ala Leu Pro Ser Trp Asp Thr Cys Asn Lys Gln Leu Pro Lys Pro
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Ala Pro Thr Thr Phe Leu Tyr Lys Val Ala Ser Asn Val
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 <213> Homo sapiens

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tgctggagag tgagcagccc tagcaggg atg gac atg atg ctg ttg gtg cag 112
 Met Asp Met Met Leu Leu Val Gln
 1 5

ggt gct tgt tgc tcg aac cag tgg ctg gcg gcg gtg ctc ctc agc ctg 160
 Gly Ala Cys Cys Ser Asn Gln Trp Leu Ala Ala Val Leu Leu Ser Leu
 10 15 20

tgc tgc ctg cta ccc tcc tgc ctc ccg gct gga cag agt gtg gac ttc 208
 Cys Cys Leu Leu Pro Ser Cys Leu Pro Ala Gly Gln Ser Val Asp Phe
 25 30 35 40

ccc tgg gcg gcc gtg gac aac atg atg gtc aga aaa ggg gac acg gcg 256
 Pro Trp Ala Ala Val Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala
 45 50 55

Sequence Listing

gtg ctt agg tgt tat ttg gaa gat gga gct tca aag ggt gcc tgg ctg	304
Val Leu Arg Cys Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu	
60 65 70	
aac cgg tca agt att att ttt gcg gga ggt gat aag tgg tca gtg gat	352
Asn Arg Ser Ser Ile Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp	
75 80 85	
cct cga gtt tca att tca aca ttg aat aaa agg gac tac agc ctc cag	400
Pro Arg Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln	
90 95 100	
ata cag aat gta gat gtg aca gat gat ggc cca tac acg tgt tct gtt	448
Ile Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val	
105 110 115 120	
cag act caa cat aca ccc aga aca atg cag gtg cat cta act gtg caa	496
Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln	
125 130 135	
gtt cct cct aag ata tat gac atc tca aat gat atg acc gtc aat gaa	544
Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu	
140 145 150	
gga acc aac gtc act ctt act tgt ttg gcc act ggg aaa cca gag cct	592
Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu Pro	
155 160 165	
tcc att tct tgg cga cac atc tcc cca tca gcg aaa cca ttt gaa aat	640
Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe Glu Asn	
170 175 180	
gga caa tat ttg gac att tat gga att aca agg gac cag gct ggg gaa	688
Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln Ala Gly Glu	
185 190 195 200	
tat gaa tgc agt gcg gaa aat gat gtg tca ttc cca gat gtg agg aaa	736
Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser Phe Pro Asp Val Arg Lys	
205 210 215	

Sequence Listing

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ggc acc gtg acc ccc gga cgc agt ggc ctg ata aga tgt gaa ggt gca Gly Thr Val Thr Pro Gly Arg Ser Gly Leu Ile Arg Cys Glu Gly Ala 235 240 245	832
ggg gtg ccg cct cca gcc ttt gaa tgg tac aaa gga gag aag aag ctc Gly Val Pro Pro Pro Ala Phe Glu Trp Tyr Lys Gly Glu Lys Lys Leu 250 255 260	880
ttc aat ggc caa caa gga att att att caa aat ttt agc aca aga tcc Phe Asn Gly Gln Gln Gly Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser 265 270 275 280	928
att ctc act gtt acc aac gtg aca cag gag cac ttc ggc aat tat act Ile Leu Thr Val Thr Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr 285 290 295	976
tgt gtg gct gcc aac aag cta ggc aca acc aat gcg agc ctg cct ctt Cys Val Ala Ala Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu 300 305 310	1024
aac cct cca agt aca gcc cag tat gga att acc ggg agc gct gat gtt Asn Pro Pro Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val 315 320 325	1072
ctt ttc tcc tgc tgg tac ctt gtg ttg aca ctg tcc tct ttc acc agc Leu Phe Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser 330 335 340	1120
ata ttc tac ctg aag aat gcc att cta caa taaattcaaa gaccataaa Ile Phe Tyr Leu Lys Asn Ala Ile Leu Gln 345 350	1170
aggcttttaa ggattctctg aaagtgctga tggctggatc caatctggta cagtttgta	1230
aaagcagcgt gggatataat cagcagtgtg tacatgggga tgatcgcctt ctgtagaatt	1290

Sequence Listing

gctcattatg taaatacttt aattctactc ttttttgatt agctacatta ccttgtgaag	1350
cagtacacat tgcctttttt ttaagacgtg aaagctctga aattactttt agaggatatt	1410
aattgtgatt tcatgtttgt aatctacaac ttttcaaaag cattcagtca tggctcgcta	1470
ggttgcaggc tgtagtttac aaaaacgaat attgcagtga atatgtgatt ctttaaggct	1530
gcaatacaag cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca	1590
tttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt cttcaaaata	1650
taacacatat ctagattttt ctgctcgcat gatattcagg tttcaggaat gagccttgta	1710
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atacaataat atttttctct ttgtctccaa ctaatataaa atgttttgct aaatcttaca	1830
atttgaaagt aaaaataaac cagagtgatc aagttaaacc atacactatc tctaagtaac	1890
gaaggagcta ttggactgta aaaatctctt cctgcactga caatgggggtt tgagaatttt	1950
gccccacact aactcagttc ttgtgatgag agacaattta ataacagtat agtaaataa	2010
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caaacattct atatcgggat gtagcagacc aatctctaaa atagctaatt cttcaataaa	2430
atctttctat atagccattt cagtgcacaa aagtaaaatc aaaaaagacc atcctttatt	2490

Sequence Listing

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gatgaagtta ccaatttcag tacacctaaa tttctacaaa tagtccccctt ttacaagttg	2790
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ttttagaaca aatatggcat ttaactttat tatttatttg cttttaagaa atattctttg	3150
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ccataataat ctacctacta gaaatagtgg tgctaccaca aaaaatgtta accatcagta	3270
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gagttaaaat acctcctctt tgtaagggtt gtaggtaaat tgaggataa actatggatg	3390
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ttagaagaga ctttcttgag tgacattttt aaatagagga ggtattcact atgtttttct	3570
gtatcacagc agcattccta gtccttaggc cctcggacag agtgaaatca tgagtattta	3630
tgagttcaat attgtcaaat aaggctacag tatttgcttt tttgtgtgaa tgtattgcat	3690

Sequence Listing

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ttatctttta atctataaca atttgtgtta gctgttcatt tcaggattat attttctaca	3870
agttccactt gtgggactcc ttttgttgc cctatttttt tttaaagaag gaagaaagaa	3930
aatgagtag cagtttaaaa atgagaatgg agagaaaaga aaaagaatga aaaggaaagg	3990
cagtaaagag ggaaaaaaaa ggaaggatgg aaggaatgaa ggaagggaagg gaggaagggg	4050
agaaggtagg aagaaagaaa ggatgagagg gaaggaagaa tcagagtatt agggtagtta	4110
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Sequence Listing

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4891

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<211> 354

<212> PRT

<213> Homo sapiens

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 20 25 30

Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn Met
 35 40 45

Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu Glu Asp
 50 55 60

Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile Ile Phe Ala
 65 70 75 80

Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser Ile Ser Thr Leu
 85 90 95

Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn Val Asp Val Thr Asp
 100 105 110

Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr Gln His Thr Pro Arg Thr
 115 120 125

Met Gln Val His Leu Thr Val Gln Val Pro Pro Lys Ile Tyr Asp Ile
 130 135 140

Ser Asn Asp Met Thr Val Asn Glu Gly Thr Asn Val Thr Leu Thr Cys
 145 150 155 160

Leu Ala Thr Gly Lys Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser

Sequence Listing

165 170 175
Pro Ser Ala Lys Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly
180 185 190
Ile Thr Arg Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp
195 200 205
Val Ser Phe Pro Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala
210 215 220
Pro Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser
225 230 235 240
Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu
245 250 255
Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile
260 265 270
Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val Thr
275 280 285
Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly
290 295 300
Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr Ala Gln Tyr
305 310 315 320
Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys Trp Tyr Leu Val
325 330 335
Leu Thr Leu Ser Ser Phe Thr Ser Ile Phe Tyr Leu Lys Asn Ala Ile
340 345 350
Leu Gln

<210> 11

Sequence Listing

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 cgtttccgag gcggggccga gggcggcgtc gctgaggcgc cc atg gcc ttc 231
 Met Ala Phe
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 gcc cgc cgg ctc ctg cgc ggg cca ctg tcg ggg ccg ctg ctc ggg cgg 279
 Ala Arg Arg Leu Leu Arg Gly Pro Leu Ser Gly Pro Leu Leu Gly Arg
 5 10 15
 cgc ggg gtc tgc gct ggg gcc atg gct ccg ccg cgc cgc ttc gtc ctg 327
 Arg Gly Val Cys Ala Gly Ala Met Ala Pro Pro Arg Arg Phe Val Leu
 20 25 30 35
 gag ctt ccc gac tgc acc ctg gct cac ttc gcc cta ggc gcc gac gcc 375
 Glu Leu Pro Asp Cys Thr Leu Ala His Phe Ala Leu Gly Ala Asp Ala
 40 45 50
 ccc ggc gac gca gac gcc ccc gac ccc cgc ctg gcg gcg ctg ctg ggg 423
 Pro Gly Asp Ala Asp Ala Pro Asp Pro Arg Leu Ala Ala Leu Leu Gly
 55 60 65
 ccc ccg gag cgc agc tac tcg ctg tgc gtg ccc gtg acc ccg gac gcc 471
 Pro Pro Glu Arg Ser Tyr Ser Leu Cys Val Pro Val Thr Pro Asp Ala
 70 75 80

Sequence Listing

ggc tgc ggg gcc cgg gtc cgg gcg gcg cgg ctg cac cag cgc ctg ctg Gly Cys Gly Ala Arg Val Arg Ala Ala Arg Leu His Gln Arg Leu Leu 85 90 95	519
cac cag ctg cgc cgc ggc ccc ttc cag cgg tgc cag ctg ctc agg ctg His Gln Leu Arg Arg Gly Pro Phe Gln Arg Cys Gln Leu Leu Arg Leu 100 105 110 115	567
ctc tgc tac tgc ccg ggc ggc cag gcc ggc ggc gca cag caa ggc ttc Leu Cys Tyr Cys Pro Gly Gly Gln Ala Gly Gly Ala Gln Gln Gly Phe 120 125 130	615
ctg ctg cgc gac ccc ctg gat gac cct gac acc cgg caa gcg ctg ctc Leu Leu Arg Asp Pro Leu Asp Asp Pro Asp Thr Arg Gln Ala Leu Leu 135 140 145	663
gag ctg ctg ggc gcc tgc cag gag gca cca cgc ccg cac ttg ggc gag Glu Leu Leu Gly Ala Cys Gln Glu Ala Pro Arg Pro His Leu Gly Glu 150 155 160	711
ttc gag gcc gac ccg cgc ggc cag ctg tgg cag cgc ctc tgg gag gtg Phe Glu Ala Asp Pro Arg Gly Gln Leu Trp Gln Arg Leu Trp Glu Val 165 170 175	759
caa gac ggc agg cgg ctg cag gtg ggc tgc gca cag gtc gtg ccc gtc Gln Asp Gly Arg Arg Leu Gln Val Gly Cys Ala Gln Val Val Pro Val 180 185 190 195	807
ccg gag ccc ccg ctg cac ccg gtg gtg cca gac ttg ccc agt tcc gtg Pro Glu Pro Pro Leu His Pro Val Val Pro Asp Leu Pro Ser Ser Val 200 205 210	855
gtc ttc ccg gac cgg gaa gcc gcc cgg gcc gtt ttg gag gag tgt acc Val Phe Pro Asp Arg Glu Ala Ala Arg Ala Val Leu Glu Glu Cys Thr 215 220 225	903
tcc ttt att cct gaa gcc cgg gca gtg ctt gac ctg gtc gac cag tgc Ser Phe Ile Pro Glu Ala Arg Ala Val Leu Asp Leu Val Asp Gln Cys 230 235 240	951

Sequence Listing

cca aaa cag atc cag aaa gga aag ttc cag gtt gtt gcc atc gaa gga	999
Pro Lys Gln Ile Gln Lys Gly Lys Phe Gln Val Val Ala Ile Glu Gly	
245 250 255	
ctg gat gcc acg ggt aaa acc acg gtg acc cag tca gtg gca gat tca	1047
Leu Asp Ala Thr Gly Lys Thr Thr Val Thr Gln Ser Val Ala Asp Ser	
260 265 270 275	
ctt aag gct gtc ctc tta aag tca cca ccc tct tgc att ggc cag tgg	1095
Leu Lys Ala Val Leu Leu Lys Ser Pro Pro Ser Cys Ile Gly Gln Trp	
280 285 290	
agg aag atc ttt gat gat gaa cca act atc att aga aga gct ttt tac	1143
Arg Lys Ile Phe Asp Asp Glu Pro Thr Ile Ile Arg Arg Ala Phe Tyr	
295 300 305	
tct ttg ggc aat tat att gtg gcc tcc gaa ata gct aaa gaa tct gcc	1191
Ser Leu Gly Asn Tyr Ile Val Ala Ser Glu Ile Ala Lys Glu Ser Ala	
310 315 320	
aaa tct cct gtg att gta gac agg tac tgg cac agc acg gcc acc tat	1239
Lys Ser Pro Val Ile Val Asp Arg Tyr Trp His Ser Thr Ala Thr Tyr	
325 330 335	
gct ata gcc act gag gtg agt ggg ggt ctc cag cac ctg ccc cca gcc	1287
Ala Ile Ala Thr Glu Val Ser Gly Gly Leu Gln His Leu Pro Pro Ala	
340 345 350 355	
cat cac cct gtg tac cag tgg cca gag gac ctg ctc aaa cct gac ctt	1335
His His Pro Val Tyr Gln Trp Pro Glu Asp Leu Leu Lys Pro Asp Leu	
360 365 370	
atc ctg ctg ctc act gtg agt cct gag gag agg ttg cag agg ctg cag	1383
Ile Leu Leu Leu Thr Val Ser Pro Glu Glu Arg Leu Gln Arg Leu Gln	
375 380 385	
ggc cgg ggc atg gag aag acc agg gaa gaa gca gaa ctt gag gcc aac	1431
Gly Arg Gly Met Glu Lys Thr Arg Glu Glu Ala Glu Leu Glu Ala Asn	
390 395 400	

Sequence Listing

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agt gtg ttt cgt caa aag gta gaa atg tcc tac cag cgg atg gag aat      1479
Ser Val Phe Arg Gln Lys Val Glu Met Ser Tyr Gln Arg Met Glu Asn
    405                410                415

cct ggc tgc cat gtg gtt gat gcc agc ccc tcc aga gaa agg gtc ctg      1527
Pro Gly Cys His Val Val Asp Ala Ser Pro Ser Arg Glu Arg Val Leu
    420                425                430                435

cag acg gta tta agc cta atc cag aat agt ttt agt gaa ccg              t      1570
Gln Thr Val Leu Ser Leu Ile Gln Asn Ser Phe Ser Glu Pro
    440                445

agttactctg gccaggtgcc acgtctaact agattagatg ttgtttgaaa catctacatc      1630

caccatttgt tatgcagtgt tcccaaattt ctgttctaca agcatgttgt gtggcagaaa      1690

actggagacc aggcatttta attttacttc agccatcgta ccctcttctg actgatggac      1750

ccgtcatcac aaagggtccct ctcatcatgt tccagtgaga ggccagcgat tgctttcttc      1810

ctggcatagt aaacattttc ttggaacata tgtttcactt aatcactacc aaatatctgg      1870

aagacctgtc ttactcagac agcaccaggt gtacagaagc agcagacaag atcttcaga      1930

tcagcagga gaccccgag cctctgcttc tctacactg gcatgctgat gagatcgtga      1990

catgcccaca ttggcttctt ccacatctgg ttgcactcgt catgatgggc tcgctgcac      2050

tccctcagtc ccaaattcta gagccaagtg ttcctgcaga ggctgtctat gtgtcctggc      2110

tgcccaagga cactcctgca gagccatttt tgggtaagga acacttaca agaaggcatt      2170

gatcttgtgt ctgaggctca gagccctttt gataggcttc tgagtcatat ataaagacat      2230

tcaagccaag atgctccaac tgcaaata ccaaccttct ctgaattata ttttgcttat      2290

ttatatttct tttctttttt tctaaagtat ggctctgaat agaatgcaca ttttcattg      2350

aactggatgc atttcattta gccaatccag taatttat atattaatct atacaatatg      2410

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Sequence Listing

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tttcctcagc ataggagcta tgattcatta attaaaagtg gagtcaaaac gctaaatgca      2470
atgtttgttg tgtattttca ttacacaaac ttaatttgtc ttgttaaata agtacagtgg      2530
atcttgaggt gggatttctt ggtaaattat cttgcacttg aatgtctcat gattacatat      2590
gaaatcgctt tgacatatct ttagacagaa aaaagtagct gagtgagggg gaaattatag      2650
agctgtgtga ctttagggag taggttgaac caggtgatta cctaaaattc cttccagttc      2710
aaaggcagat aaatctgtaa attattttat cctatctacc atttcttaag aagacattac      2770
tccaaaataa ttaaatttaa ggctttatca ggtctgcata tagaatctta aattctaata      2830
aagtttcatg ttaatgtcat aggattttta aaagagctat aggtaatctt tatataatat      2890
gtgtatatta aaatgtaatt gatttcagtt gaaagtatct taaagctgat aaatagcatt      2950
agggttcttt gcaatgtggt atctagctgt attattgggt ttatttactt taaacatctt      3010
gaaaagctta tactggcagc ctagaaaaac aaacaattaa tgtatcttta tgtccctggc      3070
acatgaataa actttgctgt gggtttact      3098

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<210> 12

<211> 449

<212> PRT

<213> Homo sapiens

<400> 12

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Met Ala Phe Ala Arg Arg Leu Leu Arg Gly Pro Leu Ser Gly Pro Leu
  1             5             10             15

```

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Leu Gly Arg Arg Gly Val Cys Ala Gly Ala Met Ala Pro Pro Arg Arg
      20             25             30

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Phe Val Leu Glu Leu Pro Asp Cys Thr Leu Ala His Phe Ala Leu Gly
      35             40             45

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Sequence Listing

Ala Asp Ala Pro Gly Asp Ala Asp Ala Pro Asp Pro Arg Leu Ala Ala
50 55 60

Leu Leu Gly Pro Pro Glu Arg Ser Tyr Ser Leu Cys Val Pro Val Thr
65 70 75 80

Pro Asp Ala Gly Cys Gly Ala Arg Val Arg Ala Ala Arg Leu His Gln
85 90 95

Arg Leu Leu His Gln Leu Arg Arg Gly Pro Phe Gln Arg Cys Gln Leu
100 105 110

Leu Arg Leu Leu Cys Tyr Cys Pro Gly Gly Gln Ala Gly Gly Ala Gln
115 120 125

Gln Gly Phe Leu Leu Arg Asp Pro Leu Asp Asp Pro Asp Thr Arg Gln
130 135 140

Ala Leu Leu Glu Leu Leu Gly Ala Cys Gln Glu Ala Pro Arg Pro His
145 150 155 160

Leu Gly Glu Phe Glu Ala Asp Pro Arg Gly Gln Leu Trp Gln Arg Leu
165 170 175

Trp Glu Val Gln Asp Gly Arg Arg Leu Gln Val Gly Cys Ala Gln Val
180 185 190

Val Pro Val Pro Glu Pro Pro Leu His Pro Val Val Pro Asp Leu Pro
195 200 205

Ser Ser Val Val Phe Pro Asp Arg Glu Ala Ala Arg Ala Val Leu Glu
210 215 220

Glu Cys Thr Ser Phe Ile Pro Glu Ala Arg Ala Val Leu Asp Leu Val
225 230 235 240

Asp Gln Cys Pro Lys Gln Ile Gln Lys Gly Lys Phe Gln Val Val Ala
245 250 255

Sequence Listing

Ile Glu Gly Leu Asp Ala Thr Gly Lys Thr Thr Val Thr Gln Ser Val
260 265 270

Ala Asp Ser Leu Lys Ala Val Leu Leu Lys Ser Pro Pro Ser Cys Ile
275 280 285

Gly Gln Trp Arg Lys Ile Phe Asp Asp Glu Pro Thr Ile Ile Arg Arg
290 295 300

Ala Phe Tyr Ser Leu Gly Asn Tyr Ile Val Ala Ser Glu Ile Ala Lys
305 310 315 320

Glu Ser Ala Lys Ser Pro Val Ile Val Asp Arg Tyr Trp His Ser Thr
325 330 335

Ala Thr Tyr Ala Ile Ala Thr Glu Val Ser Gly Gly Leu Gln His Leu
340 345 350

Pro Pro Ala His His Pro Val Tyr Gln Trp Pro Glu Asp Leu Leu Lys
355 360 365

Pro Asp Leu Ile Leu Leu Leu Thr Val Ser Pro Glu Glu Arg Leu Gln
370 375 380

Arg Leu Gln Gly Arg Gly Met Glu Lys Thr Arg Glu Glu Ala Glu Leu
385 390 395 400

Glu Ala Asn Ser Val Phe Arg Gln Lys Val Glu Met Ser Tyr Gln Arg
405 410 415

Met Glu Asn Pro Gly Cys His Val Val Asp Ala Ser Pro Ser Arg Glu
420 425 430

Arg Val Leu Gln Thr Val Leu Ser Leu Ile Gln Asn Ser Phe Ser Glu
435 440 445

Pro

Sequence Listing

<210> 13
 <211> 1893
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (418) .. (1392)
 <223> LBFL167 Clone #20

<400> 13
 agtccagctg ccgttaggcg ctgggatagt cgcacgctgg atgcatctac gtccgccgag 60
 cccctggggc gaagaggccg cgtccgcctt catttgtggc cggtgcttcg cccctgacc 120
 cttcgcccc aaagaccagc tctaactga gcgcctcggc cgccctgccc cagcctcgta 180
 cagcgcgcca gcctcgccca gccggtgtcc ggagaccctc gggccgtgtc catttgtggg 240
 caaagccagc ggggcaggct tggccagagt gcaccactcg gcgccgtccc aggcccgacg 300
 ctctggggcg gcccggaacc ccaggttcgc ggcccgtgtt tccgaccggc ggaggggggt 360
 cagcggcccc atccacgga agcgcgctcg gaggggtggg acccggccgg accggag 417
 atg gcg ccg cca gcg ggc ggg gcg gcg gcg gcc tcg gac ttg ggc 465
 Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ser Asp Leu Gly
 1 5 10 15
 tcc gcc gca gtg ctc ttg gct gtg cac gcc gcg gtg agg ccg ctg ggc 513
 Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly
 20 25 30
 gcc ggg cca gac gcc gag gca cag ctg cgg agg ctg cag ctg agc gcg 561
 Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala
 35 40 45
 gac cct gag cgg cct ggg cgc ttc cgg ctg gag ctg ctg ggc gcg gga 609
 Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly

Sequence Listing

50	55	60	
cct ggg gcg gtt aat ttg gag tgg ccc ctg gag tca gtt tcc tac acc			657
Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr			
65	70	75	80
atc cga ggc ccc acc cag cac gag cta cag cct cca cca gga ggg cct			705
Ile Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro			
85	90	95	
gga acc ctc agc ctg cac ttc ctc aac cct cag gaa gct cag cgg tgg			753
Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp			
100	105	110	
gca gtc cta gtc cga ggt gcc acc gtg gaa gga cag aat ggc agc aag			801
Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys			
115	120	125	
agc aac tca cca cca gcc ttg ggc cca gaa gca tgc cct gtc tcc ctg			849
Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu			
130	135	140	
ccc agt ccc ccg gaa gcc tcc aca ctc aag ggc cct cca cct gag gca			897
Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala			
145	150	155	160
gat ctt cct agg agc cct gga aac ttg acg gag aga gaa gag ctg gca			945
Asp Leu Pro Arg Ser Pro Gly Asn Leu Thr Glu Arg Glu Glu Leu Ala			
165	170	175	
ggg agc ctg gcc cgg gct att gca ggt gga gac gag aag ggg gca gcc			993
Gly Ser Leu Ala Arg Ala Ile Ala Gly Gly Asp Glu Lys Gly Ala Ala			
180	185	190	
caa gtg gca gcc gtc ctg gcc cag cat cgt gtg gcc ctg agt gtt cag			1041
Gln Val Ala Ala Val Leu Ala Gln His Arg Val Ala Leu Ser Val Gln			
195	200	205	
ctt cag gag gcc tgc ttc cca cct ggc ccc atc agg ctg cag gtc aca			1089
Leu Gln Glu Ala Cys Phe Pro Pro Gly Pro Ile Arg Leu Gln Val Thr			

Sequence Listing

210	215	220	
ctt gaa gac gct gcc tct gcc gca tcc gcc gcg tcc tct gca cac gtt			1137
Leu Glu Asp Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala His Val			
225	230	235	240
gcc ctg cag gtc cac ccc cac tgc act gtt gca gct ctc cag gag cag			1185
Ala Leu Gln Val His Pro His Cys Thr Val Ala Ala Leu Gln Glu Gln			
245	250	255	
gtg ttc tca gag ctc ggt ttc ccg cca gcc gtg caa cgc tgg gtc atc			1233
Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val Gln Arg Trp Val Ile			
260	265	270	
gga cgg tgc ctg tgt gtg cct gag cgc agc ctt gcc tct tac ggg gtt			1281
Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu Ala Ser Tyr Gly Val			
275	280	285	
cgg cag gat ggg gac cct gct ttc ctc tac ttg ctg tca gct cct cga			1329
Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg			
290	295	300	
gaa gcc cca ggt cag tcc tcg atg ggg gtg ggg tgt ggg agg tgg ggt			1377
Glu Ala Pro Gly Gln Ser Ser Met Gly Val Gly Cys Gly Arg Trp Gly			
305	310	315	320
gca gcc cca cag tcc	tgagctcc acccctcag ccacaggacc tagccctcag		1430
Ala Ala Pro Gln Ser			
325			
cacccccaga agatggacgg ggaacttgga cgcttgtttc ccccatcatt ggggctaccc			1490
ccaggccccc agccagctgc ctccagcctg ccagctccac tccagcccag ctggtcctgt			1550
ccttcctgca ccttcatcaa tgccccagac cgccctggct gtgagatgtg tagcaccag			1610
aggccctgca cttgggaccc ccttgctgca gcttccacct agcagccacc agaggtacca			1670
gaggtggcac aggcagggga ggtggggggc cagggcagaa tccacaggaa tgaccagct			1730

Sequence Listing

cctccccac aggttacaag gggagagtgg cccttcctc acaagtccga catctccagg 1790

cccccaactga actccgggga cctctactga ctgcttgctg ggacagtcac caggggtggg 1850

gggaaggggcc acaaaatgaa accattaaag acccttaaga gcc 1893

<210> 14

<211> 325

<212> PRT

<213> Homo sapiens

<400> 14

Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ala Ser Asp Leu Gly

1 5 10 15

Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly

20 25 30

Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala

35 40 45

Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly

50 55 60

Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr

65 70 75 80

Ile Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro

85 90 95

Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp

100 105 110

Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys

115 120 125

Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu

130 135 140

Sequence Listing

Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala
145 150 155 160

Asp Leu Pro Arg Ser Pro Gly Asn Leu Thr Glu Arg Glu Glu Leu Ala
165 170 175

Gly Ser Leu Ala Arg Ala Ile Ala Gly Gly Asp Glu Lys Gly Ala Ala
180 185 190

Gln Val Ala Ala Val Leu Ala Gln His Arg Val Ala Leu Ser Val Gln
195 200 205

Leu Gln Glu Ala Cys Phe Pro Pro Gly Pro Ile Arg Leu Gln Val Thr
210 215 220

Leu Glu Asp Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala His Val
225 230 235 240

Ala Leu Gln Val His Pro His Cys Thr Val Ala Ala Leu Gln Glu Gln
245 250 255

Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val Gln Arg Trp Val Ile
260 265 270

Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu Ala Ser Tyr Gly Val
275 280 285

Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg
290 295 300

Glu Ala Pro Gly Gln Ser Ser Met Gly Val Gly Cys Gly Arg Trp Gly
305 310 315 320

Ala Ala Pro Gln Ser
325

<210> 15

<211> 1597

<212> DNA

Sequence Listing

<213> Homo sapiens

<220>

<221> CDS

<222> (271)..(1431)

<223> LBFL167 Clone #46

<400> 15

gtgagcgcct cggccgccct gcccagcct cgtacacgcc gccagctcgc ccagccggtg 60

tccggagacc ctccggccgt gtccatttgt gggcaaagcc agcggggcag gcttgccag 120

agtgcaccac tcggcgccgt cccaggcccg acgctctggg cgcgcccgga accccaggtt 180

cgcgccccgt gtttccgacc ggccgagggg gctcagcggc ccgatccac ggaagcgcgc 240

tcggaggggt gggacccggc cggaccggag atg gcg ccg cca gcg ggc ggg gcg 294

Met Ala Pro Pro Ala Gly Gly Ala

1

5

gcg gcg gcg gcc tcg gac ttg ggc tcc gcc gca gtg ctc ttg gct gtg 342

Ala Ala Ala Ala Ser Asp Leu Gly Ser Ala Ala Val Leu Leu Ala Val

10

15

20

cac gcc gcg gtg agg ccg ctg ggc gcc ggg cca gac gcc gag gca cag 390

His Ala Ala Val Arg Pro Leu Gly Ala Gly Pro Asp Ala Glu Ala Gln

25

30

35

40

ctg cgg agg ctg cag ctg agc gcg gac cct gag agg cct ggg cgc ttc 438

Leu Arg Arg Leu Gln Leu Ser Ala Asp Pro Glu Arg Pro Gly Arg Phe

45

50

55

cgg ctg gag ctg ctg ggc gcg gga cct ggg gcg gtt aat ttg gag tgg 486

Arg Leu Glu Leu Leu Gly Ala Gly Pro Gly Ala Val Asn Leu Glu Trp

60

65

70

ccc ctg gag tca gtt tcc tac acc atc cga ggc ccc acc cag cac gag 534

Pro Leu Glu Ser Val Ser Tyr Thr Ile Arg Gly Pro Thr Gln His Glu

75

80

85

Sequence Listing

cta cag cct cca cca gga ggg cct gga acc ctc agc ctg cac ttc ctc	582
Leu Gln Pro Pro Pro Gly Gly Pro Gly Thr Leu Ser Leu His Phe Leu	
90 95 100	
aac cct cag gaa gct cag cgg tgg gca gtc cta gtc cga ggt gcc acc	630
Asn Pro Gln Glu Ala Gln Arg Trp Ala Val Leu Val Arg Gly Ala Thr	
105 110 115 120	
gtg gaa gga cag aat ggc agc aag agc aac tca cca cca gcc ttg ggc	678
Val Glu Gly Gln Asn Gly Ser Lys Ser Asn Ser Pro Pro Ala Leu Gly	
125 130 135	
cca gaa gca tgc cct gtc tcc ctg ccc agt ccc ccg gaa gcc tcc aca	726
Pro Glu Ala Cys Pro Val Ser Leu Pro Ser Pro Pro Glu Ala Ser Thr	
140 145 150	
ctc aag ggc cct cca cct gag gca gat ctt cct agg agc cct gga aac	774
Leu Lys Gly Pro Pro Pro Glu Ala Asp Leu Pro Arg Ser Pro Gly Asn	
155 160 165	
ttg acg gag aga gaa gag ctg gca ggg agc ctg gcc cgg gct att gca	822
Leu Thr Glu Arg Glu Glu Leu Ala Gly Ser Leu Ala Arg Ala Ile Ala	
170 175 180	
ggg gga gac gag aag ggg gca gcc caa gtg gca gcc gtc ctg gcc cag	870
Gly Gly Asp Glu Lys Gly Ala Ala Gln Val Ala Ala Val Leu Ala Gln	
185 190 195 200	
cat cgt gtg gcc ctg agt gtt cag ctt cag gag gcc tgc ttc cca cct	918
His Arg Val Ala Leu Ser Val Gln Leu Gln Glu Ala Cys Phe Pro Pro	
205 210 215	
ggc ccc atc agg ctg cag gtc aca ctt gaa gac gct gcc tct gcc gca	966
Gly Pro Ile Arg Leu Gln Val Thr Leu Glu Asp Ala Ala Ser Ala Ala	
220 225 230	
tcc gcc gcg tcc tct gca cac gtt gcc ctg cag gtc cac ccc cac tgc	1014
Ser Ala Ala Ser Ser Ala His Val Ala Leu Gln Val His Pro His Cys	
235 240 245	

Sequence Listing

act gtt gca gct ctc cag gag cag gtg ttc tca gag ctc ggt ttc ccg	1062
Thr Val Ala Ala Leu Gln Glu Gln Val Phe Ser Glu Leu Gly Phe Pro	
250 255 260	
cca gcc gtg caa cgc tgg gtc atc gga cgg tgc ctg tgt gtg cct gag	1110
Pro Ala Val Gln Arg Trp Val Ile Gly Arg Cys Leu Cys Val Pro Glu	
265 270 275 280	
cgc agc ctt gcc tct tac ggg gtt cgg cag gat ggg gac cct gct ttc	1158
Arg Ser Leu Ala Ser Tyr Gly Val Arg Gln Asp Gly Asp Pro Ala Phe	
285 290 295	
ctc tac ttg ctg tca gct cct cga gaa gcc cca gcc aca gga cct agc	1206
Leu Tyr Leu Leu Ser Ala Pro Arg Glu Ala Pro Ala Thr Gly Pro Ser	
300 305 310	
cct cag cac ccc cag aag atg gac ggg gaa ctt gga cgc ttg ttt ccc	1254
Pro Gln His Pro Gln Lys Met Asp Gly Glu Leu Gly Arg Leu Phe Pro	
315 320 325	
cca tca ttg ggg cta ccc cca ggc ccc cag cca gct gcc tcc agc ctg	1302
Pro Ser Leu Gly Leu Pro Pro Gly Pro Gln Pro Ala Ala Ser Ser Leu	
330 335 340	
ccc agt cca ctc cag ccc agc tgg tcc tgt cct tcc tgc acc ttc atc	1350
Pro Ser Pro Leu Gln Pro Ser Trp Ser Cys Pro Ser Cys Thr Phe Ile	
345 350 355 360	
aat gcc cca gac cgc cct ggc tgt gag atg tgt agc acc cag agg ccc	1398
Asn Ala Pro Asp Arg Pro Gly Cys Glu Met Cys Ser Thr Gln Arg Pro	
365 370 375	
tgc act tgg gac ccc ctt gct gca gct tcc acc tagcagcca ccagaggta	1450
Cys Thr Trp Asp Pro Leu Ala Ala Ala Ser Thr	
380 385	
caaggggaga gtggcccttc cctcacaagt ccgacatctc caggccccca ctgaactccg	1510
gggacctcta ctgactgctt gctgggacag tcaccagggt tggggggaag ggccacaaaa	1570

Sequence Listing

tgaaaccatt aaagaccctt aagagcc

1597

<210> 16

<211> 387

<212> PRT

<213> Homo sapiens

<400> 16

Met Ala Pro Pro Ala Gly Gly Ala Ala Ala Ala Ser Asp Leu Gly

1 5 10 15

Ser Ala Ala Val Leu Leu Ala Val His Ala Ala Val Arg Pro Leu Gly

20 25 30

Ala Gly Pro Asp Ala Glu Ala Gln Leu Arg Arg Leu Gln Leu Ser Ala

35 40 45

Asp Pro Glu Arg Pro Gly Arg Phe Arg Leu Glu Leu Leu Gly Ala Gly

50 55 60

Pro Gly Ala Val Asn Leu Glu Trp Pro Leu Glu Ser Val Ser Tyr Thr

65 70 75 80

Ile Arg Gly Pro Thr Gln His Glu Leu Gln Pro Pro Pro Gly Gly Pro

85 90 95

Gly Thr Leu Ser Leu His Phe Leu Asn Pro Gln Glu Ala Gln Arg Trp

100 105 110

Ala Val Leu Val Arg Gly Ala Thr Val Glu Gly Gln Asn Gly Ser Lys

115 120 125

Ser Asn Ser Pro Pro Ala Leu Gly Pro Glu Ala Cys Pro Val Ser Leu

130 135 140

Pro Ser Pro Pro Glu Ala Ser Thr Leu Lys Gly Pro Pro Pro Glu Ala

145 150 155 160

Sequence Listing

Asp Leu Pro Arg Ser Pro Gly Asn Leu Thr Glu Arg Glu Glu Leu Ala
165 170 175

Gly Ser Leu Ala Arg Ala Ile Ala Gly Gly Asp Glu Lys Gly Ala Ala
180 185 190

Gln Val Ala Ala Val Leu Ala Gln His Arg Val Ala Leu Ser Val Gln
195 200 205

Leu Gln Glu Ala Cys Phe Pro Pro Gly Pro Ile Arg Leu Gln Val Thr
210 215 220

Leu Glu Asp Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala His Val
225 230 235 240

Ala Leu Gln Val His Pro His Cys Thr Val Ala Ala Leu Gln Glu Gln
245 250 255

Val Phe Ser Glu Leu Gly Phe Pro Pro Ala Val Gln Arg Trp Val Ile
260 265 270

Gly Arg Cys Leu Cys Val Pro Glu Arg Ser Leu Ala Ser Tyr Gly Val
275 280 285

Arg Gln Asp Gly Asp Pro Ala Phe Leu Tyr Leu Leu Ser Ala Pro Arg
290 295 300

Glu Ala Pro Ala Thr Gly Pro Ser Pro Gln His Pro Gln Lys Met Asp
305 310 315 320

Gly Glu Leu Gly Arg Leu Phe Pro Pro Ser Leu Gly Leu Pro Pro Gly
325 330 335

Pro Gln Pro Ala Ala Ser Ser Leu Pro Ser Pro Leu Gln Pro Ser Trp
340 345 350

Ser Cys Pro Ser Cys Thr Phe Ile Asn Ala Pro Asp Arg Pro Gly Cys
355 360 365

Glu Met Cys Ser Thr Gln Arg Pro Cys Thr Trp Asp Pro Leu Ala Ala

Sequence Listing

370

375

380

Ala Ser Thr

385

<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

gctgaagcag gaaaatcgct t

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

tgagacggag tctcactcgg t

21

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

Sequence Listing

<400> 19

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24

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

cgcccaagct ttctctttt

19

<210> 21

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

caccctttgc ctctgtcact tccgca

26

<210> 22

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

Sequence Listing

<400> 22

gctggagcac caggactgca ttg

23

<210> 23

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ggagctgagc agcagtgtaa tgaa

24

<210> 24

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

gaggcctgcc tgaaggagga gcttc

25

<210> 25

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

Sequence Listing

tctggaagta gtgcagacgc ctcagg

26

<210> 26

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

agccaacgtc ggctttgtta tccagc

26

<210> 27

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27

gctgtcagat atgatggttc tggac

25

<210> 28

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 28

ccagcctcac cactgttggg ttgc

24

Sequence Listing

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 29
cattctctga gctgtattag tgt 23

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 30
cctgagctgg aatgacctgc a 21

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 31
ctttgtgttg gctgcagcca ca 22

Sequence Listing

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
tgaggagaga ctttgctgac tggt 24

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 33
gtcctgtctg gcggtgccga 20

<210> 34
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34
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Sequence Listing

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Sequence Listing

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19

INTERNATIONAL SEARCH REPORT

ernational application No.
PCT/KR2003/002161

A. CLASSIFICATION OF SUBJECT MATTER

IPC7 C12N 15/12, C07K 14/47, C12N 15/62, C07K 16/18, A61K 48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7 C12N, C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
NCBI Genbank, EMBL, Swissprot, Delphion, Pubmed "IQGAP"

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Database NCBI Genbank [on line] Accession No. AL365181, 22 Jan. 2002 Human DNA sequence from clone RP11-284F21 on chromosome 1, complete sequence	1- 9
A	Jon W. Erickson et al. " Identification of an actin cytoskeletal complex that includes IQGAP and the Cdc42 GTPase" J. Biol.Chem. Vol.272 No. 26. pp24443-24447, 26 Sep.1997	1- 33
A	Shinya Kuroda et al. " Identification of IQGAP as a putative target for the small GTPase, Cdc42 and Rac1" J. Biol. Chem. Vol.271 No.38 pp23363-23367, 20 Sep. 1996	1- 33
A	Michael W. Briggs et al. "IQGAP1-mediated stimulation of transcriptional co-activation by beta-catenin is modulated by calmodulin", J. Biol. Chem. Vol.277 No.9 pp7453-7465, 1 Mar. 2002 Cited in the application	1- 33

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

28 JANUARY 2004 (28.01.2004)

Date of mailing of the international search report

28 JANUARY 2004 (28.01.2004)

Name and mailing address of the ISA/KR



Korean Intellectual Property Office
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Republic of Korea

Facsimile No. 82-42-472-7140

Authorized officer

CHO, Myung Sun

Telephone No. 82-42-481-5594



INTERNATIONAL SEARCH REPORT

International application No.
PCT/KR2003/002161

This international Searching Authority found multiple inventions in this international application as follows:

1. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.1 and No.3, and isolated nucleic acid molecule encoding SEQ ID No.2 and No.4.

2. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.5, and isolated nucleic acid molecule encoding SEQ ID No.6.

3. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.7, and isolated nucleic acid molecule encoding SEQ ID No.8.

4. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.9, and isolated nucleic acid molecule encoding SEQ ID No.10.

5. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.11, and isolated nucleic acid molecule encoding SEQ ID No.12.

6. Claims 1-33 (in part)

Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.13 and No.15, and isolated nucleic acid molecule encoding SEQ ID No.14 and No.16.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/KR2003/002161

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item I.b of the first sheet).

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

a. type of material



a sequence listing



table(s) related to the sequence listing

b. format of material



in written format



in computer readable form

c. time of filing/furnishing



contained in the international application as filed



filed together with the international application in computer readable form



furnished subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.

PCT/KR2003/002161

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See separate sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-33 (in part)
Inventions related to an isolated nucleic acid molecule comprising SEQ ID No.1 and No.3, and isolated nucleic acid molecule encoding SEQ ID No.2 and No.4.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.